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Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VBGF. VBGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                           Gaps
                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                             Human; VEGF; vascular endothelial growth factor; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                            neovascularisation, lymphangiogenesis, psoriasis, tumour,
diabetes induced neovascular sequelae, rheumatoid arthritis,
diabetic retinopathy, chronic inflammation, cyclic.
                                                                                                                     Score 65; DB 4; Length LJ, Pred. No. 0.00033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .13
/note= "This bond cyclises the peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cendron A;
                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 25; Page 47; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                        AAU04537 standard; peptide; 13 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stacker S,
                                                                                                                                                                                                                                                                                                                                                     VEGF based monocyclic peptide 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JAN-2001; 2001WO-US001533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JAN-2000; 2000US-0176293P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-MAY-2000; 2000US-0204590P
                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                  1 CASELGKTSNTFC 13
                                                                                                                                                                                   1 CASELGKSTNTFC 13
                                                                                                                                                        11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hughes RA,
                                                                              diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-442248/47.
                                                                                                                              Query Match
Best Local Similarity
                                                                                                      Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200152875-A1
                                                                                                                                                                                                                                                                                                                            26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Achen MG,
                                                                                                                                                                                                                                                                                                   AAU04537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            residues
                                                                                                                                                         Matches
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Gaps

0;

Score 65; DB 4; Length 13, Pred. No. 0.00033;

2;

90.3%;

Query Match
Best Local Similarity 84.6
Matches 11, Conservative

diabetic retinopathy

Sequence 13 AA;

ò g

infection. The peptides are also used to modulate vacular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VeGF. VeGF-Cor. D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and

·.

characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, arknopathy, hemangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cotramms, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver

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Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                    /note= "A disulfide bond forms between residue 17 and residue 17 of an identical peptide to form a dimeric peptide"
                                                                                                                            Human; VEGF; vascular endothelial growth factor; angiogenesis;
                                                                                                                                          neovascularisation, lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.

    .13
/note= "This bond cyclises the peptide"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cendron A;
                                                                                                  VEGF based bicyclic dimeric peptide #4.
                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stacker S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LUDW-) LUDWIG INST CANCER RES.
                       AAU04547 standard; peptide; 17
                                                                                                                                                                                                                                                                                                                                                                                                                        16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                                                                                                                                                18-JAN-2001; 2001WO-US001533
                                                                                                                                                                                                                                                                                                                                                                                                            18-JAN-2000; 2000US-0176293P
                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-442248/47.
                                                                                                                                                                                                                                    Disulfide-bond
                                                                                                                                                                                                                                                             Disulfide-bond
                                                                                                                                                                                                                                                                                                                               WO200152875-A1
                                                                           26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                         26-JUL-2001
                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Achen MG,
                                                  AAU04547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     residues
                                                                                                                                                                                                                          Key
RESULT
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The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and peptides the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis,

neovascularisation or lymphangiogenesis in a mammal with a condition

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16-MAY-2000; 2000US-0204590P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU04549
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                                                                                                                         The sequence represents a classic partylic peptide of the invention, whose 3-dimensional structure is madelled on the expose loop of human veger (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta.

Deta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior peptides) and a cyclic peptide with at least one amino acid deleted prior cordisation are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis, neovascularisation or lymphangiogenesis.

The condition is diabetic retinopathy, psoriasis, arthropathy, cerebrovascular accident, post-angioplasty restenosis, head, heat or crauma, substance-induced neovascularisation of the liver, excessive trauma, substance-induced neovascularisation of the liver, excessive corporated angiogenic dysfunction, diabetes induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability cor brain. The peptides are also used to modulate vascular permeability accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are also used to inage blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation with an anti-inflammatory agent, to treat a chronic inflammation with an anti-inflammatory agent, to treat and the control of the cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ÷
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                     sequence represents a dimeric bicyclic peptide of the invention,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neovascularisation, lymphangiogenesis, psoriasis, tumour; diabetes induced neovascular sequelae, rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels

    .13
/note= "This bond cyclises the peptide"

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Pred. No. 0.00044;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VEGF based bicyclic dimeric peptide #8
     Example 26; Page 49; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CASELGKTSNTFC 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disulfide-bond
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The sequence represents a dimeric bicyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human CC whose 3-dimensional structure is modelled on the expose loop of human CC whose 1-dimensional structure is modelled on the expose loop of human CC welpot is a monomeric monocyclic peptide by a measuring beta-beta carbon separation distances on opposite antiparallel strands of a cyclising the peptide by oxidising the cyclein residues. The monocyclic peptides, dimeric bicyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis.

The condition are used to interfere with angiogenesis, or evascularisation or lymphanglogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphanglogenesis.

The condition is diabetic retinopathy, psoriasis, arthropathy, caracterised by angiogenesis, neovascularisation or lymphanglogenesis.

The condition is diabetic retinopathy, psoriasis, arthropathy, carebovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition of machines and lymphatic contamilation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain The mammal has a condition described and lymphatic or brain. The peptides are used to inmeries and lymphaters.
                                                                                                                                                                                                                           Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vasculature. The monomeric and bicyclic peptides are used to interfere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 65; DB 4; I
Pred. No. 0.00044;
                                                                         Cendron A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VEGF based bicyclic dimeric peptide #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 26; Page 49; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU04549 standard; peptide; 17 AA
                                                                             Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2;
                                                                                 Stacker
(LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.3%;
84.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CASELGKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CASELGRSTNSFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                 Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diabetic retinopathy
                                                                                                                                                  WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
tes 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                 Achen MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU04549;
                                                                                                                                                                                                                                                                                                                                                         residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chronic
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growth factor; angiogenesis;

Human, VEGF; vascular endothelial growth factor; angiogenesis neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.

VEGF based monocyclic peptide 14.

26-SEP-2001 (first entry)

13 /note= "This bond cyclises the peptide"

Location/Qualifiers

Disulfide-bond

Synthetic

WO200152875-A1 26-JUL-2001

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Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
       /note= "A disulfide bond forms between residue 17 and residue 17 of an identical peptide to form a dimeric peptide."
/note= "This bond cyclises the peptide"
                                                                                                                                           Cendron A;
                                                                                                                                                                                                                    Example 26; Page 49; 102pp; English.
                                                                                                                                            Stacker S,
                                                                                                                         (LUDW-) LUDWIG INST CANCER RES.
                                                                                 18-JAN-2001; 2001WO-US001533.
                                                                                                 18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
                                                                                                                                           Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        diabetic retinopathy
                                                                                                                                                          WPI; 2001-442248/47
        Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17 AA;
                                                 WO200152875-A1
                                                                 26-JUL-2001
                                                                                                                                          Achen MG,
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lymphangiogenesis, is produced by cyclizing a peptide loop fragment om an exposed loop of a growth factor protein by oxidizing the cysteine Novel monomeric monocyclic peptide, used to interfere with angiogenesis,

Example 25; Page 47; 102pp; English.

residues.

Cendron A;

Stacker S,

Hughes RA,

Achen MG,

WPI; 2001-442248/47.

(LUDW-) LUDWIG INST CANCER RES 18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P. 18-JAN-2001; 2001WO-US001533

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The sequence represents a dimeric bicyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human voice 3-dimensional structure is modelled on the expose loop of human version (version version of period of producing a monomeric monocyclic peptide by a measuring betactor beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis.

CC peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis.

CC peptides) and a cyclic peptide with a least one amino acid deleted prior characterised by angiogenesis, neovascularisation or lymphangiogenesis.

CC haracterised by angiogenesis, neovascularisation or lymphangiogenesis.

CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.

CC crawma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal large are used to image blood vessels and lymphatic or brain. The peptides are used to image blood vessels and lymphatic or vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or D and contain inflammation, especially rheumatoid arthritis, psoriasis and althritis, and and activity phenesus of contains and and activity induced are contained and and activity induced are contained and activity induced 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 65; DB 4; Length 17; Pred. No. 0.00044; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CASELGKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
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The sequence trappescents a micrometric monocyclic peptiae of the invention, whose 3-dimensional structure is modelled on the expose loop of human veget (vascular endothelial growth factor). The invention relates to a method of producing a monometric monocyclic peptide by a measuring betabeta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclisming the peptide by oxidiasing the growth factor protein and cyclisming the peptide by oxidiasing the separations. The monocyclic peptides, and a cyclic peptide with at least one amino acid deleted prior cyclisation are used to interfere with angiogenesis, concavacularisation or lymphangiogenesis, concaracterised by angiogenesis, neovascularisation or lymphangiogenesis, or cyclisation are used to interfere with angiogenesis, condition is diabetic retinopathy, psoriamis, arthropathy. The condition is diabetic retinopathy, psoriamis, arthropathy cerebrovascular accident, post-angioplasty restenosis, head, heat or cordition is diabetic retinopathy, psoriamis, and hear or cold tramma, substance-induced neovascularisation of the liver, excessive cordinated angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability or brain. The peptides are used to image blood vessels and lymphatic vasculation in peripheral limbs or in lumps, peritoned loving and accumulation in peripheral activity induced by VBGF, VBGF-C or D and a chronic inflammation, especially rheumatoid arthritis, psoriasis and accumulation with an anti-inflammatory agent, to treat a condition inflammation with an anti-inflammatory agent, to treat a condition with an anti-inflammator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence represents a monomeric monocyclic peptide of the invention,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 61; DB 4; Length 13;
Pred. No. 0.0016;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.7%;
ilarity 76.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diabetic retinopathy
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13 AA;
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Gaps ..

> 1 CASELGKSTNTFC 13 ::

à

AAU04536 standard; peptide; 13 AA.

RESULT 11

a

AAU04536;

AAU04536 ID AAU0. XX AC AAU0. XX

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Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                   /note= "A disulfide bond forms between residue 17 and residue 17 of an identical peptide to form a dimeric peptide"
                                                                                                                                 Human; VEGF; vascular endothelial growth factor; angiogenesis;
                                                                                                                                           neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.

    .13

'note= "This bond cyclises the peptide"

                                                                                                                                                                                                                                                                                                                                                                                                      Cendron A;
                                                                                                             VEGF based bicyclic dimeric peptide #5.
                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                      Ś
                                                 AAU04548 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                      Stacker
                                                                                                                                                                                                                                                                                                                                                                                 (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                18-JAN-2001; 2001WO-US001533
                                                                                                                                                                                                                                                                                                                                                   18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
                                                                                       26-SEP-2001 (first entry)
1 CASDVGKSTNTWC 13
                                                                                                                                                                                                                                                                                                                                                                                                      Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-442248/47.
                                                                                                                                                                                                                Disulfide-bond
                                                                                                                                                                                                                                     Disulfide-bond
                                                                                                                                                                                                                                                                                        WO200152875-A1
                                                                                                                                                                                                                                                                                                           26-JUL-2001
                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                      Achen MG,
                                                                     AAU04548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            residues
                             RESULT 12
                                         AAU04548
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dysfunction, diabetes induced neovascular sequelae, hypertension induced residues. The Begunicar Expressions a dimerric bioyello peptide by the management of the superaction, whose 3-dimensional structure is anotabiled on the expose to the invention, whose 3-dimensional structure is monografic peptide by a measuring beta-carbon separation distances on opposite antiparable strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides by oxidising the cysteine residues. The monocyclic peptides by oxidising the cyclising the peptide with at least one amino acid deleted prior peptides, dimerric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior peptides) and a cyclic peptide with a least one amino acid deleted prior cyclisation are used to interfere with angiogenesis.

CC cyclisation are used to interfere with angiogenesis.

CC cyclisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis.

CC cyclisation is diabetic retinopathy, psoriasis, arthropathy, corrections is diabetic retinopathy, psoriasis, arthropathy, corrections and angiogenesis and a condition, diabetes induced neovascular sequelac, head, heat or cord trauma, substance-induced neovascularisation of the liver, excessive corpusation. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to inage blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere The sequence represents a dimeric bicyclic peptide of the invention, Example 26; Page 49; 102pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence represents Human VEGF-D (vascular endothelial growth factor) amino acids Val101-Thr 173, used together with the C-terminal 23 residues of VEGF to make a hybrid theoretical molecule for 3 dimensional modelling. The sequence is used in a method of producing a monomeric monocyclic peptide by a measuring beta-beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, pscriasis, arthropathy, hemangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold tramma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic
with at least one biological activity induced by VBGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat chronic inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; VEGF-D; vascular endothelial growth factor; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition characterised by
                                                                                                                                                                                  ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation.
                                                                                                                                          Score 61; DB 4; Length 17; Pred. No. 0.0021; i Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cendron A;
                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human VEGF-D amino acids Val101-Thr 173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 90-91; 102pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stacker S,
                                                                                                                                                                                                                                                                                                                                                                   AAU04522 standard; protein; 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JAN-2001; 2001WO-US001533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .8-JAN-2000; 2000US-0176293P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L6-MAY-2000; 2000US-0204590P.
                                                                                                                                             84.7%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                          1 CASELGKSTNTFC 13
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                                                                                                                                               Query Match
Best Local Similarity 76.9
Matches 10; Conservative
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                                                                 diabetic retinopathy
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                                                                                                       Sequence 17 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                                                                             RESULT 13
                                                                                                                                                                                                                                                                                                                                                  AAU0452;
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neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -b and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy
                                                                                                                                                                                                                                                                                                             Sequence 73 AA;
      8X88888888X8
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75.0%; Score 54; DB 4; Length 73; 100.0%; Pred. No. 0.15; or Indels ive 0; Mismatches 0; Indels
                                 11; Conservative
                                                                2 ASELGKSTNTF 12
                                                                                              21 ASELGKSTNTF
Query Match
Best Local Similarity
                                Matches
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AAU04520 standard; protein; 96 AA.
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(first entry) 26-SEP-2001 AAU04520;

Human VEGF-D amino acids Val101-PRO186.

Human, VEGF-D; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation.

WO200152875-A1 Homo sapiens

26-JUL-2001.

18-JAN-2001; 2001WO-US001533.

18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P.

(LUDW-) LUDWIG INST CANCER RES

Hughes RA, Achen MG,

Cendron A;

Stacker S,

WPI; 2001-442248/47.

lymphangiogenesis, is produced by cyclizing a peptide loop fragment on an exposed loop of a growth factor protein by oxidizing the cysteine monomeric monocyclic peptide, used to interfere with angiogenesis, residues. Novel

Example 1; Page 89; 102pp; English.

amino acids Val101-PRO186. The sequence is used in a method of producing a monomeric represents numeral by a measuring beta-beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric by oxidising the cysteine residues. The monocyclic peptides, dimeric beptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, neovascularisation or lymphanglogenesis, neovascularisation or lymphanglogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, postsequence represents Human VEGF-D (vascular endothelial growth factor) RESULT 14
AAU04520
ID AAU041
XX
XX
DT 26-SEI
XX
DE Human
XX
DE HUM

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neovascularisation of the liver, excessive hormone related analogemic neovascularisation of the liver, excessive hormone related analogemic hydriunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF. Or D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy
angioplasty restenosis, head, heat or cold trauma,
      8.8666666666666888
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Sequence 96 AA;

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Gaps

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Gaps
                         0;
      Length 96;
                        0; Indels
    75.0%; Score 54; DB 4;
               0.2;
          100.0%; Pred. ...
Query Match
Best Local Similarity 100.
Matches 11; Conservative
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21 ASELGKSTNTF 원

31

2 ASELGKSTNTF 12

RESULT 15

AAY23889 standard; protein; 109 AA AAY23889

AAY23889;

21-SEP-1999 (first entry)

Human vascular endothelial growth factor (VEGF)-D.

Vascular endothelial growth factor; VEGF; VEGF-D; malignant melanoma; tumour; psoriasis; angiogenesis; lymphangiogenesis; skin graft; wound healing; lymphedema; scleroderma; anhydrotic ectodermal dysplasia.

Homo sapiens

WO9933485-A1.

08-JUL-1999

98WO-US027373 23-DEC-1998;

97AU-00001131 24-DEC-1997;

98US-0087392P. 29-MAY-1998;

(LUDW-) LUDWIG INST CANCER RES.

WPI; 1999-405368/34.

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Alitalo

Stacker SA,

Achen MG,

A human cell line stably expressing vascular endothelial growth factor D, useful for treating melanomas or tumors expressing ${\tt VBGF-D}$.

Claim 6; Page 72; 79pp; English.

The present sequence represents human vascular endothelial growth factor (VBGF)-D. The specification describes a human cell line which stably expresses VBGF-D, or fragments/analogues having VBGF-D biological activity. VBGF-D antagonists, e.g. antisense nucleic acids or triplex DNA, VBGF-D antagonists, e.g. antisense nucleic acids or triplex useful for the treatment or alleviation of malignant melanomas, tumours useful for the treatment or alleviation of malignant melanomas, tumours vEGF-D can be administered to enhance the acceptance and/or healing of skin grafts or to stimulate the healing of a surgical or traumatic wound to the skin. Lymphanglogenesis stimulating amounts of VBGF-D can be used to treat scleroderma. Vascularisation stimulating amounts of VBGF-D are used to treat anhydrotic ectodermal dysplasia. VBGF-D

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antibodies are useful for detecting tumours expressing VEGF-D. Fully-processed VEGF-D can be used to stimulate at least one VEGF-D bioactivity chosen from endothelial cell proliferation, migration, survival and differentiation and lymphangiogenesis without inducing vascular permeability
                                                                                                                                                                                                        Gaps
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29 ASELGKSTNTF 39
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Search completed: September 5, 2004, 09:55:09 Job time : 43.6768 sec8

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; Sequence 8, Application US/09761636A; Patent No. US20020065218A1
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Best Local Similarity
Matches 13; Conserv
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US-09-761-636A-8
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Sequence 16,
Sequence 28,
Sequence 30,
Sequence 32,
Sequence 17,
Sequence 29,
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Sequence 27,
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Sequence 3
Sequence 3
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| cgn2 6/ptodata/2/pubpaa/US07 NEW PUB.pep:*
| cgn2 6/ptodata/2/pubpaa/US06 NEW PUB.pep:*
| cgn2 6/ptodata/2/pubpaa/US06 PUBCOMB.pep:*
| cgn2 6/ptodata/2/pubpaa/US07 NEW PUB.pep:*
| cgn2 6/ptodata/2/pubpaa/US08 PUBCOMB.pep:*
| cgn2 6/ptodata/2/pubpaa/US09 PUBCOMB.pep:*
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(c) 1993 - 2004 Compugen Ltd.
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US-09-761-636A-15
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US-09-761-636A-16
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                        1 CASELGKSTNTFC 13
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Maximum DB
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Sequence 1, Appli
Sequence 3, Appli
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Sequence 11, Appl
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Sequence 119, Appl
Sequence 22, Appli
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Sequence 6, Appli
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Sequence 5, Appli
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Sequence 13, Appli
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Sequence 2, Ap
Sequence 13,
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Sequence 13,
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       S US-10-779-731-1

2 US-10-779-731-1

2 US-10-644-653-3

1 US-10-274-953-3

1 US-10-274-953-3

1 US-10-16-694-3

US-09-755-095-0

US-09-755-206A-119

US-09-755-206A-119

US-09-755-206A-119

US-09-755-206A-119

US-10-62-534B-22

US-10-62-534B-22

US-10-62-534B-22

US-10-62-534B-22

US-10-64-95-1

US-10-174-953-5

US-10-174-930-1

US-10-174-930-1

US-10-189-876-4

US-10-189-876-4

US-10-189-876-4

US-10-189-876-4

US-10-260-539-18

US-10-260-539-18

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US-10-303-9978-13
US-10-139-876-2
US-10-131-600-13
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ALIGNMENTS

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Gaps
US-09-761-636A-5

18-09-761-636A-5

18-09-761-636A-5

18-09-761-636A-5

18-09-761-636A-5

18-09-761-636A-5

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ORGANISM: Homo sapiens
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CASELGKSTNTFC

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Sequence 31, Application US/09761636A
; Sequence 31, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
    APPLICANT: ACHEN, Marc
    APPLICANT: ACHEN, Marc
; APPLICANT: BTACKER, Steven
; APPLICANT: UGHES, Richard
    APPLICANT: UGHES, Richard
    APPLICANT: CENDRON, Angela
; TITLE OF INVENTION VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REPERENCE: 1064/48505 Achen et al
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR PILING DATE: 2000-01-18
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 34
; SEQ ID NOS: 34
; SEQ ID NOS: 34
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Sequence 16, Application US/09761636A
Fatent No. US20020065218A1
GENERAL INFORMATION:
APPLICANT: ACHEN, Marc
APPLICANT: HUGHES, Richard
APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT PEPLICATION NUMBER: US/09/7fs1,636A
CURRENT PELLIG DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/176,293
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR FILE REFERENCE: 1064/48505 Achen et al CURRENT APPLICATION NUMBER: US/09/761,636A CURRENT FILING DATE: 2001-01-18 PRIOR APPLICATION NUMBER: US 60/176,293 PRIOR FILING DATE: 2000-01-18 PRIOR FILING DATE: 2000-01-18 NUMBER OF SQ. 10 NOS: 34 SOFTWARE PARENT PRIOR PRIOR FILING DATE: 2000-05-16 NUMBER OF SQ. 10 NOS: 34
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Pred. No. 3e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
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Best Local Similarity 92.3%;
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT;
CRGANISM: synthetic construct
US-09-761-636A-27
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Matches 12, Conservative
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US-09-761-636A-16
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LENGTH: 17
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Sequence 15, Application US/09761636A

Patent No. US20020065218A1

GENERAL INFORMATION:

APPLICANT: ACHEN, MAGEN

APPLICANT: HUGHES, Richard

TITLE OF INVERTION: VAGGIO-10/18

CURRENT APPLICATION NUMBER: US 60/176,293

PRIOR FILING DATE: 2000-01-18

PRIOR FILING DATE: 2000-01-18

PRIOR FILING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PATENTIN VARIENT NEIGH OF SEQ ID NOS: 34
                                                         APPLICANT: ACHEN, Marc
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: HUGHES, Richard
APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
TITLE REFERENCE: 1064/4805 Achen et al
FILE REFERENCE: 1064/4805 Achen et al
FILE REFERENCE: 2001-01-18
FRIOR PELICATION NUMBER: US 60/176,293
FRIOR PILING DATE: 2000-01-18
FRIOR PILING DATE: 2000-01-18
FRIOR PILING DATE: 2000-01-18
FRIOR PILING DATE: 2000-01-18
FRIOR FILING DATE: 2000-01-18
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100.0%; Score 72; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.7e-06;
Matches 13; Conservative 0; Mismatches 0; Indels
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Pred. No. 2.2e-05;
1; Mismatches 0; Indels
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Patent No. US20020055218A1
GENERAL INFORMATION:
APPLICANT: ACHEN, Marc
APPLICANT: HUGHES, Richard
APPLICANT: HUGHES, Richard
APPLICANT: CENDRON, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.8%;
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Best Local Similarity 92...
Local Similarity 92...
Local Similarity 12...
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                                    GENERAL INFORMATION:
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US-09-761-636A-27
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LENGTH: 13
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us-09-761-636a-5.open.rapb

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; Sequence 32, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
          ; SEQ ID NO 28
; LENGTH: 17
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-28
                                                                                                                                            90.3%;
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; ORGANISM: synthetic construct
US-09-761-636A-32
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Best Local Similarity 84.6
Matches 11; Conservative
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                                                                                                                                                                                   11; Conservative
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Best Local Similarity
Matches 11; Conserv
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US-09-761-636A-30
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US-09-761-636A-32
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Sequence 18, Application US/09761636A

Patent No. US20020065218A1

GENERAL INFORMATION:

APPLICANT: ACHEN, Marc

APPLICANT: ATCKER, Steven

APPLICANT: TAGKER, Richard

APPLICANT: CENDRON, Angela

TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR

FILE REFERENCE: 1064/48505 Achen et al

CURRENT APPLICATION NUMBER: US, 60/1761, 636A

PRIOR APPLICATION NUMBER: US, 60/176, 293

PRIOR PLING DATE: 2000-01-18

PRIOR PLING DATE: 2000-01-18

PRIOR PLING DATE: 2000-01-18

PRIOR PLING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 34

NUMBER OF SEQ ID NOS: 34
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; Patent No. US20020065218A1
; GENERAL INOORMATION:
    APPLICANT: ACHEN, Marc
    APPLICANT: STACKER, Steven
    APPLICANT: CENDRON, Angela
    TITLE OF INVENTION: VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
    FILE REFERENCE: 1064/48505 Achen et al
    CURRENT APPLICATION NUMBER: US/09/761,636A
    CURRENT PELICATION NUMBER: US 60/176,293
    PRIOR FILING DATE: 2000-01-18
    PRIOR FILING DATE: 2000-03-16
    NUMBER OF SEQ ID NOS: 34
    SOFTWARE: PatentIn Version 3.0
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Pred. No. 0.00011;
2; Mismatches 0; Indels
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Pred. No. 0.00011;
2; Mismatches 0; Indels
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PRIOR FILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: US 60/204,590
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.0
SEQ ID NO 16
LENGTH: 13
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                                                                                                                                                  TYPE: PRT
CRGANISM: synthetic construct
US-09-761-636A-16
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Best Local Similarity 84.6
Matches 11; Conservative
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Best Local Similarity 84.6
Matches 11; Conservative
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US-09-761-636A-18
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LENGTH: 13
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Patent No. US20020065218A1

GENERAL INFORMATION:
APPLICANT: ACHEN, Marc

APPLICANT: STACKER, Steven
APPLICANT: CENDRON, Angela
ITILE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A

CURRENT APPLICATION NUMBER: US 60/176,293
PRIOR PILING DATE: 2000-01-18
PRIOR PLING DATE: 2000-01-18
PRIOR PLING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34

SEQ ID NO 30
LENGTH: 17
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APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: CENESC, Richard
APPLICANT: CENESC, Richard
APPLICANT: CENESC, Achen et al
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT PILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN VETSION 3.0
SEQ ID NO 32
LENGTH: 17
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    Length 17;
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                                                   Indels
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Score 65; DB 9; Le
Pred. No. 0.00015;
2; Mismatches 0;
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Pred. No. 0.00015;
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Gaps
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; Sequence 1, Application US/09761636A
; Parent No. US20020665218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: AUGHES, Steven
APPLICANT: HUGHES, Richard
APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEFTIDOMIMETIC INHIBITOR
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEFTIDOMIMETIC INHIBITOR
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEFTIDOMIMETIC INHIBITOR
; TILE REFERENCE: 1064/48505 Achen et al
; CURRENT PLILOTATION NUMBER: US/09/761,636A
; CURRENT PLILOG DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PALENTIN VEFFION 3.0
                                                                                                                                                                         | Sequence 3, Application US/09761636A |
| Sequence 3, Application US/09761636A |
| Patent No. US202002065218A1 |
| GENERAL INFORMATION: |
| APPLICANT: ACIBN, Marc |
| APPLICANT: ATACKER, Steven |
| APPLICANT: HUGHES, Richard |
| APPLICANT: CENDENON, Angela |
| TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR |
| FILE REPRENCE: 1064/48505 Achen et al |
| CURRENT APPLICATION NUMBER: US/09/761,636A |
| CURRENT FILING DATE: 2001-01-18 |
| PRIOR PPLICATION NUMBER: US 60/176,293 |
| PRIOR FILING DATE: 2000-01-18 |
| PRIOR FILING DATE: 2000-05-16 |
| NUMBER OF SEQ ID NOS: 34 |
| SEQ ID NO 3 |
| LENGTH: 73 |
| LENGTH: 73 |
| CONTINENT OF THE NOS: 34 |
| CONTINENT OF 
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Best Local Similarity 100.0
Matches 11; Conservative
                              1 CASDVGKSTNTWC 13
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Matches 11; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-09-761-636A-1
                                                                                                                                                            RESULT 13
US-09-761-636A-3
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| Sequence 29, Application US/09761636A |
| Patent No. US20020065218A1 |
| GENERAL INFORMATION: |
| APPLICANT: ACHEN, Marc |
| APPLICANT: BIGGRES, Richard |
| APPLICANT: CENDRON, Angela |
| TITLE OF INVENTION: USGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR |
| TITLE OF INVENTION: USGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR |
| TITLE OF INVENTION: USGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR |
| FILE REFERENCE: 1064/48505 Achen et al. 36A |
| CURRENT FILING DATE: 2001-01-18 |
| PRIOR APPLICATION NUMBER: US 60/176,293 |
| PRIOR PILING DATE: 2000-01-18 |
| PRIOR PILING DATE: 2000-01-18 |
| PRIOR PILING DATE: 2000-05-16 |
| NUMBER OF SEQ ID NOS: 34 |
| NUMBER OF SEQ ID NOS: 34 |
| SOFTWARE: PATENTIN VETSION 3.0
                                                                                                                                                                                                                                                                                                                                                                           Sequence 17, Application US/09761636A

Sequence 17, Application US/09761636A

Patent No. US2020065218A1

GENERAL INFORMATION:
APPLICANT: ACHEN, WARE
APPLICANT: CENDROW, Angel
APPLICANT: CENDROW, Angel
CURRENT FILITE OF INVENTION: VECF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT FILING DATE: 2000-101-18
PRIOR PILING DATE: 2000-101-18
PRIOR PILING DATE: 2000-01-18
PRIOR PILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34

SOFTWARE: Patentin version 3.0

SEQ ID NO 17

LENGTH: 13
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Pred. No. 0.00059;
3; Mismatches 0; Indels
                                        Length 17;
                              Score 65; DB 9; I Pred. No. 0.00015; 2; Mismatches 0;
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                                        90.3%;
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Best Local Similarity 76.9%;
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Best Local Similarity 76.9
Matches 10; Conservative
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                                     Query Match
Best Local Similarity 84.6
Matches 11; Conservative
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US-09-761-636A-29
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US-09-761-636A-17
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Sequence 3, Application US/09956095

Fatent No. US20020102260A1

GENERAL INFORMATION:

APPLICANT: ACHEN, MACG G.

TITLE OF INVENTION: WESCULAR ENDOTHELIAG GROWTH FACTOR D EXPRESSION, FOR SCREENING

TITLE OF INVENTION: VASCULARIZATIC DISEASE CHARACTERIZED BY

TITLE OF INVENTION: VASCULARIZATIC DISEASE OR METASTATIC RISK AND FOR MAINTAINING

TITLE OF INVENTION: VASCULARIZATION OF TISSUE

FILE REFERENCE: 1064/48666PC

CURRENT APPLICATION NUMBER: US/09/956,095

FILE REFERENCE: 1000-09-20

PRIOR APPLICATION NUMBER: 60/234,196

PRIOR APPLICATION NUMBER: 60/234,196

PRIOR PLING DATE: 2000-09-20

PRIOR FILING DATE: 2000-09-20

PRIOR FILING DATE: 2000-09-20

WUMBER OF SEQ ID NOS: 4

SOFTWARE: PATENTIAN OF SEQ ID NOS: 4

SOFTWARE: PATENTIAL 109

TYPE: PRT

**CRANISM: Homo sapiens

US-09-956-095-3
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75.0%; Score 54; DB 9; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.095;
Matches 11; Conservative 0; Mismatches 0; Indels
2 ASELGKSTNTF 12
                            21 ASELGKSTNTF 31
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US-09-956-095-3
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Search completed: September 5, 2004, 10:29:18 Job time: 37.5051 secs

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                                                                                             5, 2004, 09:55:30 ; Search time 11.5556 Seconds (without alignments) 58.079 Million cell updates/sec
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Sequence 8,
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Sequence 5,
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Sequence 1
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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US-09-431-988-8

US-08-915-795-3

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US-09-986-119-3

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US-08-467-955-1

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US-08-891-848-13

US-08-394-268-1

US-09-394-268-1

US-09-394-268-1

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US-09-394-268-1

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                                                                                                                                                                                                                                                                                      389414 seqs, 51625971 residues
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                                                             OM protein - protein search, using sw model
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                1 CASELGKSTNTFC 13
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Maximum DB seq length: 200000000
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 US-09-469-185-1

US-09-469-185-1

Sequence 1, Application US/09469185

Patent No. 6531185

GENERAL INFORMATION:

APPLICANT: ACHEN, Marc G.

APPLICANT: STACKER, Steve A.

ITILE OF INVENTION: ANTIBODIES TO TRUNCATED VEGF-D AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/469,185

CURRENT APPLICATION NUMBER: US/09/469,185

CURRENT PILING DATE: 1999-12-21

EARLIER APPLICATION NUMBER: 60/113,254

EARLIER PILING DATE: 1999-05-17

SARLIER PILING DATE: 1999-05-17

NUMBER OF SEQ ID NOS: 1

SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                              41,49,
 61,
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APPLICANT: ACKEN, MAIC G.
APPLICANT: STACKER, Steve A.
TITLE OF INVENTION: ANTIBODIES TO TRUNCATED VEGF-D AND USES THEREOF
FILE REPERENCE: ACKEN 1044-44660
CURRENT APPLICATION NUMBER: U5/09/469,186
CURRENT APPLICATION NUMBER: 60/113,254
EARLIER PILING DATE: 1998-12-21
EARLIER PLING DATE: 1999-12-21
EARLIER PLING DATE: 1999-05-17
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Pred. No. 0.047;
0; Mismatches 0; Indels
US-08-875-811-26
US-08-875-811-39
US-08-875-811-28
US-08-875-811-20
US-08-875-811-32
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US-08-875-811-57
US-08-875-811-57
US-08-875-811-57
US-08-875-811-57
US-08-875-811-57
US-08-875-811-57
US-08-875-811-57
US-08-875-811-55
US-08-875-811-55
                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                     Sequence 1, Application US/09469186
Patent No. 6383484
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 75.0%; Scc
1 Similarity 100.0%; Pr
11; Conservative 0;
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SEQ ID NO 1
LENGTH: 109
TYPE: PRT
        2 ASELGKSTNTF 12
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US-09-469-186-1
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75.0%; Score 54; DB 3; Length 325; 100.0%; Pred. No. 0.14; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C. STREET: 1200 G Street, NW, Suite 700 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,795
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REGISTRATION NUMBER: 1064/42983
TELEPRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAX: (202) 628-8800
TELEPRAX: (202) 628-8844
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                FILING DATE:
CLASSIFICATION: 536
ATTORNEY, AGENT INFORMATION:
NAME: EVANS, JOSEPh D.
REGISTRATION NUMBER: 26,269
REPERENCE/DOCKET NUMBER: 1064/42983
TELECOMMUNICATION INFORMATION:
TELEFHONE: (202) 628-8840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08915795;
Patent No. 6235713;
GENERAL INFORMATION:
APPLICANT: Marc G. ACHEN
APPLICANT: Steven A. STACKER
APPLICANT: Steven A. STACKER
APPLICANT: Steven A. STACKER
TILLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington STATE: DC COUNTRY: United States of America ZIP: 20005
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATING SYSTEM: PC-DOS/MS-DOS
                        SOFTWARE: Patentin Release #1.0, N
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: N/A INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                             TELEX: N/A
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
TISSUE TYPE: Human Breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                354 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 ASELGKSTNTF 12
                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL:
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Sequence 8, Application US/09431888A
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wise, LIV.
APPLICANT: Fleming, Stephen
APPLICANT: Stacker, Stephen
TITLE OF INVENTION: VASCULAR ENOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF
TITLE OF INVENTION: VASCULAR ENOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF
TITLE OF INVENTION: RECEPTOR-2, AND USES THEREOF
FILE REFERENCE: Sequence Listing for 09/431,833
Patent No. 6541008
                                                                                                                                                           Gaps
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US-08-915-795-3
US-08-915-795-3
; Sequence 3, Application US/08915795
; Patent No. 6235713
; APPLICANT:
APPLICANT: Andrew F. WILKS
APPLICANT: Steven A. STACKER
APPLICANT: ALITALO
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: 1200 G Street, NW, Suite 700
STREET: 1200 G Street, NW, Suite 700
STREET: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 75.0%; Score 54; DB 4; Length 197; 1 Similarity 100.0%; Pred. No. 0.086; 11; Conservative 0; Mismatches 0; Indels
                                                                                                                 Length 109;
                                                                                           Score 54; DB 4; Lengtu LV.; Pred. No. 0.047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/431,888A
CURRENT FILING DATE: 1999-11-02
EARLIER APPLICATION NUMBER: 60/106,689
EARLIER FILING DATE: 1998-11-02
EARLIER FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 8
SEQ ID NO 8
                                                                                                          ch 75.0%; Score 54; DB 1 Similarity 100.0%; Pred. No. 0.(11; Conservative 0; Mismatches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45 ASELGKSTNTF 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
CORGANISM: Homo sapiens
US-09-431-888-8
                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-469-185-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 11; Conserv
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Best Local Similarity
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        LENGTH: 109
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Query Match
Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                           RESULT 6
US-08-915-795-9
; Sequence 9, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: ALLITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bvenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
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Pred. No. 0.16;
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Pred. No. 0.46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,795
                                                                                                                             75.0%; Scor.
100.0%; Pred. No. v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 106
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26, 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.8%;
90.9%;
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                                                                        ORIGINAL SOURCE:
TISSUE TYPE: Human Lung
US-08-915-795-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 321 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: Protein
ORIGINAL SOURCE:
TISSUE TYPE: Mouse Lung
US-08-915-795-9
                                                                                                                                                                          Conservative
                                                                                                                                                                                                                          121 ASELGKSTNTF 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
             STRANDEDNESS: single
TOPOLOGY: linear
                                          MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 ASELGKSTNTF 12
                                                                                                                        Query Match
Best Local Similarity
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Best Local Similarity
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.8%; Score 51; DB 3; Length 358; 90.9%; Pred. No. 0.52; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USS-08-875-811-2

SEQUENCE 2, Application US/08875811

Patent No. 6045710.

GENERAL INFORMATION:

APPLICANT: Newton, Dianne L.

APPLICANT: Modawer, Alexander

TITLE OF INVENTION: Recombinant Ribonuclease Proteins

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                          GENERAL INFORMATION:
APPLICANT: Marc G. ACHEN
APPLICANT: Andrew F. WILKS
APPLICANT: Steven A. STACKER
APPLICANT: Kari ALITALO
ITILE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & STREET: 1200 Street, NW, Suite 700
                                                                                                                                                                                                                                                                                                                               United States of America
                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
REGISTRATION NUMBER: 26,269
TELECOMMUNICATION INPORMATION:
TELEFRAX: (202) 628-8840
TELEFAX: (202) 628-8844
TELEFAX: N/A
INFORMATION FOR SEQ ID NO: 8:
US-08-915-795-8
; Sequence B, Application US/08915795
; Patent No. 6235713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 358 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TISSUE TYPE: Mouse Lung
US-08-915-795-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 ASELGKTTNTF 136
                                                                                                                                                                                                                                                                                                                        COUNTRY: United Stat. ZIP: 20005
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 ASELGKSTNTF 12
                                                                                                                                                                                                                                                                                CITY: Washington
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Gaps
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Sequence 3, Application US/09986119
Patent No. 6653104
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
Newton, Dianne L.
Goldenberg, David M.
TITLE OF INVENTION: Immunotoxins Directed Against Malignant
Cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: 1BM PC compatible

COMPUTER: 1BM PC COMPATIBLE

COMPUTER: 1BM PC COMPATIBLE

CORPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/986,119

FILING DATE: 01-NO. 6653104-2001

CLASSIFFCATION NUMBER: US/09/071,672

FILING DATE: 01-MAY-1998

APPLICATION NUMBER: US 60/046,895

FILING DATE: 02-MAY-1997

ATTORNEY/AGENT INFORMATION:

NAME: Weber: Ellen Lauver:

REGISTRATION NUMBER: 32,762

REFERENCEY/COCKET WUMBER: 32,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.7%; Score 43; DB 4; Length 83; 61.5%; Pred. No. 2.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
  FILING DATE: 02-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber: Ellen Lauver:
REGISTRATION NUMBER: 32.762
REFERENCE/DOCKET NUMBER: 015280-32510US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
INFORMATION POR SEQ ID NO: 3: SEQUENCE GHARACTERISTICS:
LENGTH: 83 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
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TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 61.5-
Local Similarity 61.5-
Local Similarity 61.5-
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                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Protein
LOCATION: 1..83
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                           TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-986-119-3
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; Sequence 3, Application US/09071672
; Sequence 3, Application US/09071672
; Patent No. 6395276
; GENERAL INFORMATION:
    APPLICANT: Rybak, Susanna M.
    APPLICANT: Gells
    NUMBER OF INVENTION: Cells
    NUMBER OF SEQUENCES: 3
    CORRESPONDENCE ADDRESS:
    ADDRESSE: Townsend and Townsend and Crew LLP
    STREET: Two Embarcadero Center, Eighth Floor
    CITY: San Francisco
    STATE: California
    COUNTRY: USA
    CONPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC Compatible
    COMPUTER: Patentin Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
    FILING DATE: 01-MAY-1998
    CLASSIFICATION DATA:
    FILING DATE: 01-MAY-1998
    CLASSIFICATION DATA:
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            COMPUTER: REALABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: W PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATPOINTY APPLICATION NUMBER: 015280-244100US
TELEPRAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 83 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43; DB 3;
Pred. No. 2.6;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 59.7%;
Best Local Similarity 61.5%;
Matches 8; Conservative 1
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CASELGKSTNTFC 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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us-09-761-636a-5.open.rai

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TELEX: No. 5595734 Applicable INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 104 amino acids TYPE: AMINO ACID
                         ORGANISM: Rana pipiens
DEVELOPMENTAL STAGE: Embryo
US-08-283-971-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Rana pipiens
DEVELOPMENTAL STAGE: Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 718-625-0399
TELEFAX: 718-625-0399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 5
                                                                                                59.7%;
illarity 61.5%;
Conservative
                                                                                                                                                                                             75 CKYKLKKSTNKFC 87
                                                                                                                                                                     1 CASELGKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-terminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CASELGKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein HYPOTHETICAL: N
                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jay, Mark H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: N
FRAGMENT TYPE: N
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-07-921-619-1
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                                                                                                                                                                                                                                                                       Gaps
                                                                                                                      LOCATION: 1..83
OTHER INFORMATION: /note= ""onc protein", positions 16-98
of SEQ ID NO:1"
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08283971

Patent No. 552975

GENERAL INFORMATION

APPLICANT: Ardelt Ph.D, Wojciech J.

APPLICANT: Mikulski, Stanislaw M.

TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: Mark H. Jay, P.C.

STREET P.O. Box 020083, General Post Office

CITY: Brooklyn

STATE: New York
                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                              59.7%; Score 43; DB 4; Length 83; 61.5%; Pred. No. 2.6; tive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASIPICATION: 435
RICOR APPLICATION DATA:
APPLICATION NUMBER: US 07/178,118
FILING DATE: 30-UUL-1992
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
FILING DATE: 10-APR-1988
FILING DATE: 13-NOV-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZUP: 11202-002
ZUP: 11202-002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/283,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Jay, MARK H.
REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 5006 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 718-625-0399
TELEFAX: NO. 552-0399
TELEFAX: NO. 552-0399
TELEFAX: NO. 552-0399
                TYPE: amino acid
STRANDEDNESS: <Unknown>
LENGTH: 83 amino acids
                                                                                                    NAME/KEY: Protein
                                          TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acid
TYPE: amino acid
                                                                                                                                                                                                                          Query Match
Best Local Similarity 61.57
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                           60 CKYKLKKSTNKFC 72
                                                                                                                                                                                                                                                                                                   1 CASELGKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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ANTI-SENSE: N
FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
US-08-283-971-1
                                                                                                                                                                                           US-09-986-119-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                RESULT 12
US-07-921-619-1
; Sequence 1, Application US/07921619
; Patent No. 555734
; GENERAL INFORMATION:
APPLICANT: Ardelt Ph.D, Wojciech J.
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark H. Jay, P.C.
STREET: PO. Box 020083, General Post Office
CITY: Brooklyn
STATE: New York
                          Gaps
                          ٠.
Score 43; DB 1; Length 104;
Pred. No. 3.3;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.7%; Score 43; DB 1; Length 104; 61.5%; Pred. No. 3.3; tive 1; Mismatches 4; Indels
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0

Gaps

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HYPOTHETICAL: N
ANTI-SENSE: N
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                          US-08-467-95-1

Sequence 1, Application US/08467955

FRACER NO. 5728005

GENERAL INFORMATION:
PARACHEL Ph.D, Wojciech J.

ITTLE OF INVENTION: PHENVACEUTICALS AND METHOD FOR MAKING THEM NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
PADRESSEE: Mark H. Jay, P.A.

STRUE: New Jersey

COUPTY: USA

ZIP: O'0707-033

COMPUTER: New Jersey

COMPUTER: USA

ZIP: O'0707-033

COMPUTER: LUBA PCC COMPACINDE

MEDIUM TYPE: COMPUTER: USA

COMPUTER: USA

COMPUTER: USA

PELING DATE: OG-NEW-1988

FILING DATE: OG-NEW-1989

FILING DATE: US-NEW-1988

FILING DATE: US-NEW-1989

FILING DATE: US-NEW-1989
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Pred. No. 3.3;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 5007 US
TELECOMMUNICATION INFORMATION:
TELEFANN: 201-912-9066
TELEFAX: 201-912-9066
TELEFAX: 00.912-9066
TELEFAX: No. 5728805 Applicable
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 61.5%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 104 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE:
STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CASELGKSTNTFC 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Rana pipiens
DEVELOPMENTAL STAGE: O
| :| |||| ||
75 CKYKLKKSTNKFC 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE: NORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
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Sequence A. Application US/08467955

Patent No. 572805041

ONDERLY MACADIL PR.D. WOJCIGCH J.

TILLE OF INTERTION. PRACEDITICALS AND METHOD FOR MAKING THEM NUTBER CORRESPONDED.

ANDESSEE A. DESSEE MARK H. Jay. P.A.

ANDESSEE MARK H. Jay. P.A.

COMPUTER INDEADLE FORD.

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RESULT 14

Query Match
S9.7%; Score 43; DB 2; Length 104;
Best Local Similarity 61.5%; Pred. No. 3.3;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 CASELGKSINTFC 13

Db 75 CKYKLKKSTNKFC 87
Search completed: September 5, 2004, 10:21:56
Job time: 12:5556 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

; Search time 6.14141 Seconds 5, 2004, 09:47:29 September Run on:

(without alignments) 125.302 Million cell updates/sec

US-09-761-636A-6 46 Perfect score:

1 CNEESLIC 8 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283366 seqs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ovine vascular end vascular endotheli Ca2+-transporting polyketide synthas hypothetical prote probable nucleopor probable cation ef Cytcotrome P450 ib L-aspartate oxidas retinoblastoma bin probable antigenic transcription init LPS biosynthesis R glioblastoma RING laminin beta-1 cha hypothetical prote hypothetical prote vascular endotheli hypothetical prote protein-glutamate conserved hypothet vascular endotheli vascular endotheli glioma-derived vas vascular endotheli vascular endotheli uncharacterized co vascular endotheli malate dehydrogena Description SUMMARIES A33787 B49530 S57956 B40080 A45761 PN0637 T42421 T50074 H71078 T51421 I78879 B44881 A35987 A44881 AF0123 D69143 JC7562 MMHUB1 S76289 E72459 S52130 A41551 E86465 A82206 B72321 Query Match Length DB 78.3 788.3 788.3 768.3 76.1 75.0 73.9 73.9 73.9 73.9 71.7 71.7 Score Result Š.

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Gaps

0

78.3%; Score 36; DB 2; Length 133; 75.0%; Pred. No. 12; 1; Mismatches 1; Indels

Best_Local Similarity 75.0 Matches 6; Conservative

Query Match

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1-de0xv-D-xv]	malate debydrogens	malate debydrogens	hypothetical prote	malate debydrogona	majate dehydrogens	malate dehydrogens	malate debudrogens	malate dehidrogena	malace deligation	marare denydrogena	nrobable binace vo	himothetical prote	altonial transfers	himothotical mate	nypotherical proce protein F23B2.4 [i
H87486	JH0151	S13588	T16656	S17781	DEMZMC	S20743	\$52268	533066	538346	T15416	AF0118	AG0179	H97186	T21306	H88772
7	N	7	N	~	н	7	7	~	(N	7	7	~	~	101
399	429	429	429	430	432	432	435	441	441	463	765	166	1044	1047	1124
9.69	9.69	9.69	9.69	9.69	9.69	9.69	9.69	9.69	9.69	9.69	9.69	9.69	9.69	69.6	9.69
32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	thelial growth factor (version 1) by primigenius taurus (cattle) r-1990 #sequence_revision 16-Mar-15 A33787 Gospodarowicz, D.; Mitchell, R.; hys. Res. Commun. 165, 1198-1206, ular endothelial growth factor: a umber: A33787; MUID:90121225; PMID: A33787 Jiminary pe: mRNA 120 cTIS> ences: GB:M33750; NID:g163810; PIDN lternative splicing
	Query Match Query Match Best Local Similarity 75.0%; Pred. No. 11; Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
·	Oy 1 CNESLIC 8
	RESULT 2 B49530 vascular endothelial growth factor homolog A2R, 14.7K - Orf virus C;5pecies: Orf virus C;5pecies: Orf virus C;Accession: B49530 R;Vytle, D.J.; Fraser, K.M.; Fleming, S.B.; Mercer, A.A.; Robinson, A.J. J. Virol. 68, 84-92, 1994 A;Title: HOmologs of vascular endothelial growth factor are encoded by the poxvirus orf A;Reference number: A49530; MUID:94076465; PMID:8254780 A;Contents: NZ A;Accession: B49530 A;Status: preliminary A;Molecule Yrpe: DNA A;Residues: 1-133 clry- A;Cross-references: GB:S67520; NID:9456897; PIDN:AAB29220.1; PID:9456899 A;Note: sequence inconsistent with nucleotide translation A;Note: sequence extracted from NCBI backbone (NCBIN:141420, NCBIP:141425)

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1 CNEESLIC 8
                                                                    A;Accession: A45761
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1115 <MUR>
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A,Status: preliminary
A,Molecule type: DNA
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R/Tischer, E.; Gospodarowicz, D.; Mitchell, R.; Silva, M.; Schilling, J.; Lau, K.; Crisp Biochem. Biophys. Res. Commun. 165, 1198-1206, 1989
A. Fittle: Vascular endothelial growth factor: a new member of the platelet-derived growth A. Reference number: A33787; MUID:90121225; PMID:2610687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 27-190 <TIS>
A;Cross-references: GB:M31836; NID:g163808; PIDN:AAA30804.1; PID:g163809
A;Cross-references: GB:M31836; NID:g163808; PIDN:AAA30804.1; PID:g163809
B;Chem. 10.; Henzel, W.J.
Biochem. Piuophes Res: Commun. 161, 851-858, 1989
A;Title: Piuophes Res: Commun. 161, 851-858, 1989
A;Title: Piuophes: A33255; MUID:89286596; PMID:2735925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 05-Nov-1999
C;Accession: B40080; B33787; Ā33255
R;Leung, D.W.; Cachianes, G.; Kuang, W.J.; Goeddel, D.V.; Ferrara, N.
Science 246, 1306-1309, 1989
A;Title: Vascular endothelial growth factor is a secreted angiogenic mitogen.
A;Reference number: A40080; MUID:90069608; PMID:2479986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Residues: 27-31 <FER>
C;Keywords: alternative splicing; glycoprotein
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-190/Product: vascular endothelial growth factor #status predicted <MAT>
F;100/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                (domestic sheep)
#text_change 05-Nov-1999
                                                                                                                                                                                                                                                                       A;Molecule_type: mRNA
A;Residues: 1-146 <RED>
A;Cross-references: EMBL:X89506; NID:g899350; PIDN:CAA61677.1; PID:g899351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vascular endothelial growth factor precursor (version 2) - bovine
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                                                                                                                                                                                                                                                                                                                                                                               Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A45761
Ca2+-transporting ATPase (EC 3.6.3.8) - Plasmodium yoelii
C;Species: Plasmodium yoelii
ovine vascular endothelial growth factor - sheep (species: Ovis orientalis aries, Ovis ammon aries (dome: C.Species: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text. C.Accession: S57956 #sequence_revision 01-Mar-1996 #text. R.A.Redmer. D.A.; Dai, Y.; Li, J.; Jones, S.C.; Moor, R.M. R.B.Dmitted to the EMBL Data Library, July 1995 A.Reference number: S57956 A.Recession: S57956
                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36; DB 2
Pred. No. 16;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         h
Similarity 75.0%; Pred. No. 3
6; Conservative 1; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.3%;
ilarity 75.0%;
Conservative 1
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CNDESLEC 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-190 < LEU>
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
                                                                                                                                                                                                                                              A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Accession: A33255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: B40080
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Matches
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Cipate; 01-044-1931 #sequence_revision 01-30m-1939 #text_change 19-Apr-2002
Cirate: 01-044-1931 #sequence_revision 01-30m-1939 #text_change 19-Apr-2002
Cirated Extractive of a Plasmodiu world gene-encoded protein homologous to the Ca(2+)-Aprille Structure of a Plasmodiu world gene-encoded protein homologous to the Ca(2+)-Aprille Structure of a Plasmodiu world gene-encoded protein homologous to the Ca(2+)-Aprille Structure of a Plasmodiu world gene-encoded protein homologous to the Ca(2+)-Aprille Structure of a Plasmodiu world green enjage and an include signification of the Ca(2+)-Aprille Structure of a Plasmodiu world green enjage and an include signification of the Ca(2+)-Aprille Structure of a Plasmodiu world gene-encoded protein homology ARN
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5; Conservative

Local Similarity

Matches

Query Match

1205 CNEEGQVC 1212

1 CNEESLIC 8

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R; Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch. DNA Res. 5, 55-76, 1998
A; Title: Complete sequence and gene organization of the genome of a hyper-thermophilic; A; Reference number: A1000; MUID: 98344137; PMID: 9679194
A; Accession: H71078
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Residues: 1-295 < KAWA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oyrochrome P450 ib - rabbit

N.Contains: oxidoreductase (EC 1.-.-.)

S.Species: Ovytcologus cuniculus (domestic rabbit)

C.Species: Ovytcologus cuniculus (domestic rabbit)

C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000

C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000

R.Kikuta, Y.; Sogawa, K.; Haniu, M.; Kinosaki, M.; Kusunose, E.; Nojima, Y.; Yamamoto, S.

J. Biol. Chem. 266, 17821-17825, 1991

J. Biol. Chem. 266, 17821-17825, 1991

A.Reference number: A40938; WUID:92011499; PMID:177443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Note: this accession replaces an interim accession for a sequence replaced by GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AP000004; NID:g3236131; PIDN:BAA29990.1; PID:g3257307
                                                                                                                                                                                               probable cation efflux system protein czcD - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L-aspartate oxidase-like protein - Arabidopsis thaliana
N;Alternate names: protein T913_60
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C;Accession: T51421
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A/Molecule type: mRNA
A/Residues: 1-501 <KIK>
A/Cross-references: GB:D90405; NID:g217717; PIDN:BAA14401.1; PID:g217718
C/Genetics:
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C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F;308-469/Domain: cytochrome P450 homology cCYP>
F;447/Binding site: heme iron (Cys) (axial ligand) #status predicted
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73.9%; Score 34; DB 1; Length 501;
Best Local Similarity 85.7%; Pred. No. 89;
Matches 6; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: zinc transporter ZnT-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: strain OT3
                                     1748 CNEESLIDAIC 1758
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es 5; Conserv
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Best Local S:
Matches 5
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C;Superfamily: Bacillus subtilis polyketide synthase pksL; 3-oxoacyl-[acyl-carrier-prote C;Keywords: acyltransferase; carrier protein F;843-758[Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS1>F;1410-1591/Domain: short-chain alcohol dehydrogenase homology <SAD1>F;1486-2252/Domain: acyl carrier protein dehydrogenase homology <OAS2>F;2485-2559/Domain: acyl carrier protein homology <ACP1>F;2485-2559/Domain: acyl carrier protein homology <ACP2>F;2783-3181/Domain: acyl carrier protein homology <ACP2>F;2783-3181/Domain: short-chain alcohol dehydrogenase homology <SAD2>F;3576-3774/Domain: acyl carrier protein homology <ACP3>F;3852-3922/Domain: acyl carrier protein homology <ACP3>F;3852-3922/Domain: acyl carrier protein homology <ACP3>F;3892-4372/Domain: acyl carrier protein homology <ACP3>F;3892-4372/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
142421
hypothetical protein - fission yeast (Schizosaccharomyces pombe) (fragment)
C;Species: Schizosaccharomyces pombe
C;Bate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C;Accession: 142421
R;Yoshioka, S; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A;Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A;Reference number: 217323; MUID:98162722; PMID:9501991
A;Reference number: 217323; MUID:98162722; PMID:9501991
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-351 < YOS>
A;Cross-references: EMBL:DB9145; NID:91749497; PIDN:BAA13807.1; PID:91749498
A;Experimental source: strain PR745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-1778 <MCD>
A;Residues: 1-1778 <MCD>
A;Cross-references: EMBL:AL133357; PIDN:CAB62415.1; GSPDB:GN00066; SPDB:SPAC1486.05
A;Experimental source: strain 972h(-); cosmid c1486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 3.7e+02;
1; Mismatches 2; Indels
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Pred. No. 53;
0; Mismatches 0;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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62.5%;
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Best Local Similarity 72.7%;
Matches 8; Conservative (
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Query Match Best Local Similarity Matches 8; Conserv

A;Gene: SPDB:SPAC1486.05 A;Map position: 1

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A; Molecule type: mRNA
A; Residues: 1-190 < BRES
A; Cross-references: GB:S38083; MID:g249858; PIDN:AAB22253.1; PID:g249859
A; Cross-references: embryo
A; Note: sequence extracted from NCBI backbone (NCBIN:107622, NCBIP:107623)
A; Claffey, K. P; Wilkiason, W.O.; Spiegelman, B.M.
J. Biol. Chem. 267, 16317-16322, 1992
A; Title: Vascular endothelial growth factor. Regulation by cell differentiation and acti
A; Reference number: A43351; MUID:92355593; PMID:1644816
                                                                                                                                                                                                                                                                                      A,Accession: A43351
A,Molecule type: mRNA
A,Residues: 1-116, ER, 119-190 < CLA>
A,Residues: 1-116, ER, 119-190 < CLA>
A,Crose-references: GB:M95200; NID:g202350; PIDN:AAA40547.1; PID:g202351
A,Crose-references: GB:M95200; NID:g202350; PIDN:AAA40547.1; PID:g202351
A,Note: sequence extracted from NCBI backbone (NCBIN:110665, NCBIP:110675)
B,Rosenthal, R.A.; Megyesi, J.F.; Henzel, W.J.; Ferrara, N.; Folkman, J.
Growth Factors 4, 53-59, 1990
A,Title: Conditioned medium from mouse sarcoma 180 cells contains vascular endothelial gA,Reference number: A61029; MUID:91197543; PMID:2085441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 27-38 <ROS>
C;Keywords: alternative splicing; angiogenesis; dimer; disulfide bond; glycoprotein; mit
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Pred. No. 60;
2; Mismatches 1; Indels
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62.5%;
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Best Local Similarity 62.5
Matches 5; Conservative
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86 CNDEALEC 93
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C.Species: Mus musculus (house mouse)
C.Date: 03-Feb-1994 #sequence revision 03-Feb-1994 #text_change 05-Nov-1999
C.Accession: B4881; A43351; A61029
R.Breier, G.; Albrecht, U.; Sterrer, S.; Risau, W.
Development 114, 521-532, 1992
A.Aitle: Expression of vascular endothelial growth factor during embryonic angiogenesis A;Reference number: A44881; MUID:92274860; PMID:1592003
R;Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew submitted to the Protein Sequence Database, August 2000
A;Reference number: 225394
A;Recession: T51421
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-642 <SAT>
A;Cross-references: EMBL:Al391149
A;Residues: 1-642 <SAT>
A;Cross-references: EMBL:Al391149
A;Reperimental source: cultivar Columbia; BAC clone T9L3
C;Genetics:
A;Map position: 5
A;Antrons: 43/2: 158/3; 239/3; 278/3; 299/2
A;Introns: 43/2: 158/3; 239/3; 278/3; 299/2
A;Note: T9L3_60
C;Superfamily: fumarate reductase flavoprotein; 3-oxosteroid 1-dehydrogenase homology; f
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A.Residues: 1-1722 <FAT>
A.Coss-references: GB:866431; NID:g435777; PIDN:AAB28544.1; PID:g435778
R.Defeo-Jones, D.; Huang, P.S.; Jones, R.E.; Haskell, K.M.; Vuocolo, G.A.; Hanobik, M.G. Nature 352, 251-254, 1918
A.Title: Cloning of cDNAs for cellular proteins that bind to the retinoblastoma gene propression: S16953; MUID:91312450; PMID:1857421
A.Accession: S16954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cyaccesion: I78879; S16954
Syfattes, A.R.; Helin, K.; Dembaki, M.S.; Dyson, N.; Harlow, E.; Vuocolo, G.A.; Hanobik Oncogene B, 3149-3156, 1993
A;Title: Characterization of the retinoblastoma binding proteins RBP1 and RBP2.
A;Title: Characterization of the retinoblastoma binding proteins RBP1 and RBP2.
A;Reference number: IS8383; MUID:94020841; PMID:8414517
A;Accession: I78879
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
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/Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 73.9%; Score 34; DB 2; Length 642 Best Local Similarity 50.0%; Pred. No. 1.1e+02; Matches 4; Mismatches 0; Indels
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A;Map position: 3q21-3qter
C;Superfamily: human retinoblastoma binding protein 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Status: not compared with conceptual translation A,Molecule type: mRNA A,Residues: 1102-1562, 'KKK' <DEF>
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154 CDEETVVC 161
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Glioma-derived vascular endothelial cell growth factor - rat C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Nov-1990 #sequence_revision 16-Nov-1990 #text_change 05-Nov-1999
C;Coccession: 435987
R;Conn, G.; Bayne, M.L.; Soderman, D.D.; Kwok, P.W.; Sullivan, K.A.; Palisi, T.M.; Hope Proc. Natl. Acad. Sci. U.S.A. 87, 2628-2632, 1990
A;Title: Amino acid and cDNA sequences of a vascular endothelial cell mitogen that is h A;Reference number: A35987; MUID:90207249; PMID:2320579
A;Accession: A35987
A;Accession: A35987
A;Accession: Braliminary
A;Molecule type: mRNA
A;Residues: 1-190 ccon>
A;Acsidues: 1-190 ccon>
A;Cross-references: GB:M32167; NID:9204287; PIDN:AAA41211.1; PID:9204288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vascular endothelial growth factor-3 precursor - mouse N; Contains: vascular endothelial growth factor-2; vascular permeability factor C; Species: Nus musculus (house mouse) C; Species: Nus musculus (house mouse) C; Accession: A44881; C44881; A60932; S52136 C; Accession: A44881; C44881; A60932; S52136 C; Accession: A44881; C44881; A60932; S52136 M. A. Bereier, G.; Albrecht, U.; Sterrer, S.; Risau, W. Abbrecht, U.; Sterrer, S.; Risau, W. A; Title: Expression of vascular endothelial growth factor during embryonic angiogenesis A; Reference number: A44881; MUID: 92274860; PMID: 1S92003
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A;Molecule type: mRNA
A;Rebidues: 1-214 cRRE>
A;Cross-references: GB:S37052; NID:g249856; PIDN:AAB22252.1; PID:g249857
A;Experimental source: embryo
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Best Local Similarity 62.5%; Pred. No. 60;
Matches 5; Conservative 2; Mismatches 1; Indels
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A;Note: sequence extracted from NCBI backbone (NCBIN:104677, NCBIP:104678)
A;Accession: C44881
A;Accession: C44881
A;Accession: C44881
A;Accession: C44881
A;Cross-references: GB:S38100; NID:G249860; PIDN:AAB22254.1; PID:G249861
A;Accession: GB:S38100; NID:G249860; PIDN:AAB22254.1; PID:G249861
A;Accession: Mod. 172, 1535-1545, 1990
A;Title: Vascular permeability factor: a tumor-derived polypeptide that induces endothel A;Reference number: A60932; MUID:91079755; PMID:2258694
A;Accession: A60932
A;Accession: A60932
A;Molecule content Accession: Accession: Accession: Accession: Accession: Accession: Accession of MulD:91079755; PMID:2258694
A;Residues: 27-33 «CLA»
B;Sugihara, T.; Kaul, S.C.; Mitsui, Y.; Wadhwa, R.
B;Sugihara, T.; Kaul, S.C.; Mitsui, Y.; Wadhwa, R.
B;Sugihara, T.; Kaul, S.C.; Mitsui, Y.; Wadhwa, R.
B;Colim Biophys. Accession of multiple forms of VEGF is associated with spontaneous im A;Reference number: S52136; MUID:95101726; PMID:7803491
A;Reterence number
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Search completed: September 5, 2004, 10:01:16 Job time: 8.14141 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

September 5, 2004, 09:38:39 ; Search time 3.6365 Seconds (without alignments) 114.554 Million cell updates/sec Run on:

US-09-761-636A-6 46 1 CNEESLIC 8 Title: Perfect score: Sequence:

Scoring table:

141681 seqs, 52070155 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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Productions A. C., Tournead J., Schmutz J., Myeze R.M.,

Productions A. C., Tournead J., Schmutz J., Myeze R.M.,

Britaricial Y. S., N. Krzywicki M.I., Skalak U. Smailus D.E.,

Britaricial Y. S., N. Krzywicki M.I., Skalak U. Smailus D.E.,

Schnerch A., Schein J.E., Jones G.J.M., Marra M.A.,

Britaricial M. S. N. Krzywicki M.I., Skalak U. Smailus D.E.,

Schnerch A., Schein J.E., Jones G.J.M., Marra M.A.,

Britaric M. S., Sterwer K.L., Caesar C., Vitali M., Domagala T.,

MINGLINE-1001141 PubMed-10154249,

Racker S.A., Sterwers K.L., Caesar C., Vitali M., Domagala T.,

Mittalo K., Achen M.G. et al., Sterwers K.L., Caesar C., Vitali M., Domagala T.,

Alitalo K., Achen M.G. et al., Sterwers K.L., Caesar C., Vitali M., Domagala T.,

Alitalo K., Achen M.G. et al., Sterwers K.L., Caesar C., Vitali M., Domagala T.,

Alitalo K., Achen M.G. et al., Sterwers K.L., Caesar C., Worlt R. N. Kapten T.,

Alitalo K., Achen M.G. et al., Sterwers K.L., Caesar C., Contain M. Politalo K. Achen M.G. et al., Sterwers M.G.
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                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
growth factor (VEGF-D) (c-fos induced growth factor) (FIGF).
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
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                         4 X 16 AA REPEATS OF C-X(10)-C-X-C-
      VASCULAR ENDOTHELIAL GROWTH FACTOR
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                                                                                                                                                                             Score 46; DB 1; Length 354; pred. No. 0.083;
                                                                                                                                                                                                 0; Indels
                                                                                                                                                             40444 MW; 2048D769D735173E CRC64;
OR 99 (IN A MINOR FORM)
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                                                                                                                                                                                                  0; Mismatches
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                                                                                                                                                                 354 AA;
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ID VEGD_RAT
AC 035251;
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        InterPro; IPR004153; CXCX repeat.
InterPro; IPR00072; PD growth_factor.
Ffam, PF03128; CXCXc; 1.
Pfam, PF03128; DDGF; 1.
Pr0Dom; PD001629; PD growth_factor; 1.
Pr0Dom; PD001629; PD growth_factor; 1.
PR0SITE; PS00249; PDGF; 1.
PR0SITE; PS00249; PDGF; 1.
PR0SITE; PS00249; PDGF; 1.
Angiogenesis; Mitofen; Growth factor; Glycoprotein; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Orf virus (strain NZ2) (OV NZ-2).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94076465; PubMed=8254780;
Lyttle D.J., Fraser K.M., Fleming S.B., Mercer A.A., Robinson A.J.,
"Homologs of vascular endothelial growth factor are encoded by the
                                                                                                                                                                                           POTENTIAL.

4 X 16 AA REPEATS OF C-X(10)-C-X-C-X(1,3)-C.
                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLUNAC. .) (POTENTIAL).
N-LINKED (GLUNAC. .) (POTENTIAL).
N-LINKED (GLUNAC. .) (POTENTIAL).
                                                                                                                                                                                VASCULAR ENDOTHELIAL GROWTH FACTOR

    Virol. 68:84-92(1994).
    FUNCTION: INDUCES ENDOTHELIAL PROLIFERATION.
    SUBUNIT: Homodimer; disulfide-linked (By similarity).
    SIMILARITY: Belongs to the PDGF/VEGF growth factor family.

                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB 1; Length 326;
                                                                                                                                                                                                                                                                                                                               INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                    1261AFA373596C00 CRC64;
                                                                                                                                 Cleavage on pair of basic residues; Multigene family. SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Vascular endothelial growth factor homolog precursor.
                                                                                                                                                                                                                                      (APPROXIMATE)
                                                                                                                                                                                                                                                                            (INCOMPLETE)
                                                                                                                                                                                                                                                                                      BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.2;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 AA
                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                  37112 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                             87.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; S67520; AAB29220.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                              278
2298
3317
158
194
196
1150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  poxvirus orf virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CNEESLIC 8
HSSP; P15692; 1VPP
                                                                                                                                                                                                                                                                                                                                                                                                 326 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parapoxvirus.
NCBI_TaxID=10259;
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94
211
227
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                                                                                                                                                                                                                                                                                      DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                             PROPEP
CHAIN
                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                             REPEAT
REPEAT
REPEAT
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                                                                                                                                                                                        PROPEP
                                                                                                                                                                                                                                REPEAT
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VEGH_ORFN2
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
à
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SEQUENCE FROW N.A.

TISSUE-Kidney;

MEDLINE-97117958; PubMed=8958842;

Redmer D.A., Dai Y., Li J., Charnock-Jones D.S., Smith S.K.,

Redmer D.A., Dai Y., Li J., Charnock-Jones D.S., Smith S.K.,

R. Redmer D.A., Dai Y., Li J., Charnock-Jones D.S., Smith S.K.,

R. Tactor (VEGP) in the ovine corpus luteum.";

J. Reprod. Fertil. 108157-165 (1996).

CC chock factor active in angiogenesis, vasculogenesis and endothelial cell growth It induces endothelial cell growth. It induces endothelial cell migration, inhibits apoptosis, and proliferation, promotes cell migration, inhibits apoptosis, and conditionabilization of blood vessels. It binds to the profferal promotes permeabilization of blood vessels. It binds to the UGFRI/Flt-1 and VEGFRI/Kdr receptors and to heparan sulfate and heparin (By similarity).

CC SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer CC with PIGF (By similarity).

CC SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Enropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial or send an email to licensee agreement (see http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ovis aries (Sheep).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
110-OCT-2003 (Rel. 42, Last annotation update)
Vascular endothelial growth factor A precursor (VEGF-A) (Vascular VEGF OR VEGFA.
                                                                                                                                                                        POTENTIAL, VASCULAR ENDOTHELIAL GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                      ·,
                                                                                                                                                                                                                                                                                                                                                             Score 36; DB 1; Length 133;
Pred. No. 2.9;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                          INTERCHAIN (BY SIMILARITY)
INTERCHAIN (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                    133 AA; 14715 MW; 917C0F6883030C39 CRC64;
                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC
                                                                                                               PROSITE; PS00249; PDGF 1; 1.
PROSITE; PS50278; PDGF 2; 1.
Mitogen; Growth factor; Glycoprotein; Signal.
                                                                                                                                                                                                                          BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
            InterPro; IPR002400; GF cysknot.
InterPro; IPR000072; PD_growth_factor.
Pfam; PP00341; PDGF; 1.
                                                               PRINTS, PRO0438; GFCYSKNOT.
ProDom; PD001629; PD growth factor; 1.
SMART; SM00141; PDGF; 1.
                                                                                                                                                                                                            HOMOLOG
                                                                                                                                                                                                                                                                                                                                                             78.3%;
75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovidae, Caprinae, Ovis.
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                          61
70
85
                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 CNDESLEC 78
                                                                                                                                                                                                                                                                                                                                                                                                                               1 CNEESLIC 8
 HSSP; P15692; 1VPP
                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VEGA_SHEEP
ID VEGA_SHEEP
AC P50412;
                                                                                                                                                                                                                     DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                        DISULFID
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                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                      SIGNAL
                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Gaps

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0; Indels

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PRINTS; PR00438; GFCYSKNOT.
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                                                                                                                 DISULFID
                                                                                                      DISULFID
                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                    P15691;
                                                                                                                                                                                                                                                                            VEGA BOVIN
                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                     RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                with PIGF (By similarity). Substituted but remains associated to cells or to the extracellular matrix unless released by heparin (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berse B.;
Submitted (JAN-1992) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Growth factor active in angiogenesis, and endothelial cell growth. Induces endothelial proliferation and vascular permeability (By similarity).
-!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             (Vascular permeability
                                                                                                                                            BY SIMILARITY.
VASCULAR ENDOTHELIAL GROWTH FACTOR A.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
MA: 4E792CB557F91760 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cavia porcellus (Guinea pig).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Hystricognathi; Cavidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity).
SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
                                                                                                                                                                                                                                                                                  ·;
       PIR; S57956; S57956.
HSSP: P156921 1VPP.
InterPro; IPR002400; GF_Cy8knot.
InterPro; IPR00172; PD_growth_factor.
Pfam; PF00341; PDGF; 1.
PRINTS; PR00438; GFVSKNOT.
SMANT; SM00141; PDGF; 1.
PROSITE; PS00249; PDGF; 1.
PROSITE; PS00249; PDGF; 1.
PROSITE; PS00249; PDGF2; 1.
Mitogen; Anglogenesis; Growth factor; Glycoprotein; Signal; Mitogen; Anglogenesis; Growth factor; Glycoprotein; Signal;
                                                                                                                                                                                                                                                          78.3%; Score 36; DB 1; Length 146; 75.0%; Pred. No. 3.1;
                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Vascular endothelial growth factor A (VEGF-A)
                                                                                                                                                                                                                                                                      Pred. No. 3.1;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        164 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR002400; GF_cysknot.
Interpro; IPR000072; PD_growth_factor.
                                                                                                                             Heparin-binding; Multigene family SIGNAL
                                                                                                                                                                                                                                        17247 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M84230; AAA37057.1; -.
                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00341; PDGF; 1.
                                                                                                                                                  26
146
93
127
129
                                                                                                                                                                                                                                                                                                                                  CNDESLEC 93
                                                                                                                                                                                                                                                                                                           1 CNEESLIC 8
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                        146 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE=Bile duct;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10141;
                                                                                                                                                                     51
82
86
76
76
85
                                                                                                                                                                                                                                                                                                                                                                                                                                                             factor) (VPF)
VEGF OR VEGFA.
                                                                                                                                                                                                                                                                                                                                                                                          VEGA CAVPO
P26617;
                                                                                                                                                           CHAIN
DISULFID
DISULFID
                                                                                                                                                                                            DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
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MEDLINE=89286596; PubMed=2735925;
MEDLINE=89286596; PubMed=2735925;
MEDLINE=89286596; PubMed=2735925;
MEDLINE=89286596; PubMed=2735925;
Ppituitary follicular cells secrete a novel heparin-binding growth factor specific for vascular endothelial cells.";
Biochem. Biophys. Res. Commun. 161:861-8861(989).
-: FUNCTION: Growth factor active in angiogenesis, vasculogenesis and endothelial cell growth. It induces endothelial cell promite cell migration, inhibits apportosis, and induces permeabilization of blood vessels. It binds to the VEGFRI/Fit-1 and VEGFRI/Kdr receptors and to heparan sulfate and heparin (By.similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               with PIGF (By similarity). SubCELLULLAR LOCATION: Secreted but remains associated to cells or to the extracellular matrix unless released by heparin (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90121225; PubMed=2610687;
Tischer E., Gospodarowicz D., Mitchell R., Silva M., Schilling J.,
Liau K., Crisp T., Fiddes J.C., Abraham J.A.;
"Vascular endothelial growth factor: a new member of the platelet-
derived growth factor gene family.";
Biochem. Biophys. Res. Commun. 165:1198-1206(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus (Bovine).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AFR-1990 (Rel. 14, Created)
01-AFR-1990 (Rel. 14, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
pscular endothelial growth factor A precursor (VEGF-A) (Vascular VEGF OR VEGFA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 27-47.
MEDLINE=90069608; PubMed=2479986;
Leung D.W., Cachianes G., Kuang W.-J., Goeddel D.V., Ferrara N.;
"Vascular endothelial growth factor is a secreted angiogenic
                                                                                                            wth factor; Glycoprotein.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
WHY 9EB86A81A9D5DCA4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
0
                                                                                                                                                                                                                                                                                                                                                                          78.3%; Score 36; DB 1; Length 164; 75.0%; Pred. No. 3.6; 1; Indels :ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 27-190 FROM N.A. (ISOFORMS ALPHA AND BETA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing, Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 AA
ProDom; PD001629; PD_growth_factor; 1.
SMART; SM00141; PDGF; 1.
                                                                                                                                     PROSITE; PS00249; PDGF 1; 1.
PROSITE; PS50278; PDGF 2; 1.
Mitogen; Anglogenesis; Growth
DISULFID 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 246:1306-1309(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                      75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 CNDESLEC 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CNEESLIC 8
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9913;
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us-09-761-636a-6.open.rsp

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tamily.
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10-0CT-2003 (Rel. 42, Last annotation update)
Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced
growth factor) (FIGF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          VASCULAR ENDOTHELIAL GROWTH FACTOR A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
                                       Isoid=P15691-2; Sequence=VSP 004613, VSP 004614; SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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MEDLINE=97030254; PubMed=8876195;
Orlandini M., Marconcini L., Ferruzzi R., Oliviero S.;
"Identification of a c-fos-induced gene that is related to the
                                                                                                                                                                                                                                                                                                          PRONTS; PROGES, CECYSKNOT.
Probom; PRO01629; PD_growth_factor; 1.
SMART; SMO0141; PGGF; 1.
PROSITE; PSO0249; PGGF_2; 1.
PROSITE; PSS0278; PGGF_2; 1.
Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal; Hepartin-binding; Alternative splicing; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB 1; Length 190;
Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERCHAIN (BY SIMILARITY)
INTERCHAIN (BY SIMILARITY)
N-LINKED (GLCNAC. ) (POT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (in isoform Beta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -> K (in isoform Beta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EDBF903E46E24789 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        004613.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  004614
                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        358 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
               IsoId=P15691-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FTIG=VSP
                                                                                                                                                                                                                                                                      InterPro; IPR002400; GF cysknot.
InterPro; IPR000072; PD_growth_factor.
Pfam; PF00341; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /FTId=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Missing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190 AA; 22310 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                       EMBL; M32976; AAA30502.1; --
EMBL; M31836; AAA30804.1; --
EMBL; M33750; AAA30805.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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190
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127
129
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                                                                                                                                                                                                                                 PIR; A33787; A33787.
PIR; B40080; B40080.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CNEESLIC 8
                                                                                                                                                                                                                                                            HSSP; P15692; 1VGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
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82
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76
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                            Name=Beta;
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RAY RECEPTIVE SPECIFICITY.

RAY RECEPTIVE SPECIFICITY.

RAY BEDINDE-21276411; PubMed=11279005;

Raidwin M.E., Catimel B., Nice B.C., Roufail S., Hall N.E.,

Steevers K.L., Karkkainen M.J., Alitalo K., Stacker S.A., Achen M.G.;

RT actor-d is different in mouse and man.";

RI factor-d is different in mouse and man.";

Biol. Chem. 276:19166-19171(2001).

CC -!- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis and endothelial cell growth, stimulating their proliferation and underthal also has effects on the permeability of blood vessels. May function in the formation of the venous and lymphatic migration and also has effects on the permeability of blood vessels. May function in the formation of the venous and lymphatic coff differentiated lymphatic endothelium in adults. Binds and activates VEGFR-3 (FIE4) receptor.

CC of differentiated lymphatic endothelium in adults. Binds and activates VEGFR-3 (FIE4) receptor.

CC of differentiated lymphatic endothelium in adults. Binds and activates VEGFR-3 (FIE4) receptor.

CC of differentiated lymphatic endothelium in adults. Binds and activates SPECIFICITY: Highly expressed in fetal and adult lung.

CC of differentiated lymphatic endothelium in deveral body structures and organs of the embryo such as limb buds,

CC of specificity of ganglion, teeth, heart, anterior pituitary as well as countied ganglion, teeth, heart, anterior pituitary as well as vertebral column.

C1 INDUCTION: By the transcription factor c-fos.

C2 of variety of processed secreted forms with increased activity toward variety of processed secreted forms with increased activity toward linked by disulfide bonds before secretion. The fully processed control by non-covalent interactions (By similarity).

C1 inked by disulfide bonds before secretions (By similarity).

C2 in SIMILARITY: Belongs to the PDGFVUSF growth factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                  MEDLINE=98288130; PubMed=9622638; Avantaggiato V., Orlandini M., Acampora D., Oliviero S., Simeone A.; Bembryonic expression pattern of the murine figf gene, a growth factor belonging to platelet-derived growth factor/vascular endothelial growth factor family."; Mech. Dev. 73:221-224(1998).
platelet-derived growth factor/vascular endothelial growth factor
                                                                                                                                                                   Yamada Y., Nezu J.-I., Shimane M., Hirata Y.;
"Molecular cloning of a novel vascular endothelial growth factor,
                                               Proc. Natl. Acad. Sci. U.S.A. 93:11675-11680(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO, GO:0005576; C:extracellular; IDA.
GO; GO:0008083; R:growth factor activity; IDA.
GO; GO:0008515; R:protein binding; IPI.
GO; GO:0008528; P:protein binding; IPI.
GO; GO:0008283; P:cell proliferation; IDA.
InterPro; IPR04153; CXCXC_repeat.
InterPro; IPR060072; PD_growth_factor.
Pfam; PF03128; CXCXC; 2.
Pfam; PF03128; CXCXC; 2.
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                                                                                                                        TISSUE=Lung;
MEDLINE=97349118; PubMed=9205122;
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EMBL; D89628; BAA14002.1; -.
HSSP; P15692; 1VPP.
PWMA-2DPAGE; P97946; -.
                                                                                                                                                                                                                                            Genomics 42:483-488 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:108037; Figf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RECEPTOR SPECIFICITY
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                                                                                                    SEQUENCE FROM N.A.
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NCBI_TaxID=1423;
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Q05470;
                                                                                        SEQUENCE
                                                                                                            Query Match
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                                                                                                                                                                                             RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                             Strongylocentrotus purpuratus (Purple sea urchin).
Bukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoidea, Euechinoidea, Echinacea, Echinoida, Strongylocentrotidae,
                                                                                                                                                                                                                                                       Gaps
    Bryan J., Kane R.E.; "Separation of the major components of sea urchin "Separation and interaction of the major components of sea urchin
                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDINE-94022326; PubMed-8415664;
Bryan J., Edwards R.H., Matsudaira P., Otto J., Wulfkuhle J.;
"Fascin, an echinoid actin-bundling protein, is a homolog of the
                                                                                                                                                                  INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
(HOTENTIAL).
(G36B17FBF07037C CRC64;
                                                                                 4 X 16 AA REPEATS OF C-X(10)-C-X-C-X(1,3)-C.
1 (APPROXIMATE).
                                                                 VASCULAR ENDOTHELIAL GROWTH FACTOR
                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Actin polymerization and interaction with other proteins in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        temperature-induced gelation of sea urchin egg extracts.", J. Cell Biol. 71:704-714(1976).
J. Cell Biol. 71:708-714(1976).
J. PUNCTION: ACTS AS AN ACTIN BUNDLING PROTEIN.
-1- SIMILARITY: Belongs to the fascin family.
                                                                                                                                                                                                                                    DB 1; Length 358;
                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Fascin, an echinoid actin-bundling protein, is a
Drosophila singed gene product.";
Proc. Natl. Acad. Sci. U.S.A. 90:9115-9119(1993).
                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                          495 AA
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                              Pred. No. 8;
2; Mismatches
                                                                                                                                                                                                                                      78.3%; Score 36; 62.5%; Pred. No. 8
                                                                             POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                    40908 MW;
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   SMART; SM00141; PDGF; 1
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210
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CNEEGVMC 158
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NCBI_TaxID=7668;
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Best Local Similarity
Matches 5; Conserv
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SEQUENCE
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KA KUDLINE=YOU44035; FUDWEGE=39843//;

RA ALORE F., OGASAWATA N., MOSZET I., Albertini A.M., Alloni G.,

KANDER F., OGASAWATA N., MOSZET I., Bolotin A., Borchert S.,

RA ACEVEGO V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

Borlise R., Boursier L., Brans A., Eraun M., Brignell S.C. Bron S.,

RA Broullet S., Bruschi C.V., Caldwell B., Capunov V., Carter N.M.,

RA Broullet S., Bruschi C.V., Caldwell B., Capunov V., Carter N.M.,

RA Friz C., Pujita M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

RA Guiseppi G., Guy B.J., Haga K., Halech J., Grandi G.,

RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,

RA Hibbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Horita K., Lapidus K., Lardhoos Y., Klaerr-Blanchard M., Klein C.,

RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Moore D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

RA Persecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Sadaie Y.,

RA Sekiguchi J., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

RA Sekiguchi J., Sakowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,

RA Sekiguchi J., Tamaka T., Tarpstra P., Tognoni A.,

RA Takeuchi M., Tamakoshi A., Tanaka T., Tarpstrae P., Tognoni A.,

RA Tosato V., Uchiyama S., Vandendo M., Vannier F., Vassarotti A.,

Viari A., Wambutt R., Wedler B., Wedler H., Weitzenegger T.,

RA Winners P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
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MEDLINE=93345624; PubMed=8344529;
Scotti C., Piatti M., Cuzzoni A., Perani P., Tognoni A., Grandi Galizzi A., Albertini A.M.;
"A Bacillus subtilis large ORF coding for a polypeptide highly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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Pred. No. 18;
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PKSL OR PKSX OR PKSA OR OUTG OR BSU17190.
                                                                                                                                                                                                                                                                                                                                                           EMBL; L12047; AAC37183.1; -.
InterPro; IPR008999; Actin_crosslink.
Actin-binding.
INIT_MET
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Gene 130:65-71(1993).
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MEDLINE=98044033; PubMed=9384377;
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75.0%;
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Les 6; Conservative
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STANDARD;

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 Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A., "The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                          Multifunctional enzyme; Repeat; Complete proteome.
80 ACYL CARRIER (ACP) 1.
                                                                   Grandi G.;
Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: POTENTIALLY INVOLVED IN SOME INTERMEDIATE STEPS FOR THE SYNTHESIS OF A POLYKETIDE MOLECULE WHICH MAY BE INVOLVED IN SECONDARY METABOLISM.
                                                                                                                                                                                                                                    BETA-KETOACYL SYNTHASE 4.
PHOSPHOPANTETHEINE (POTENTIAL).
PHOSPHOPANTETHEINE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHOPANTETHEINE (POTENTIAL)
PHOSPHOPANTETHEINE (POTENTIAL)
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Pred. No. 1.7e+02;
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ACYL CARRIER (ACP) 4.
BETA-KETOACYL SYNTHASE 3.
BETA-KETOACYL REDUCTASE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BETA-KETOACYL REDUCTASE 1.
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BETA-KETOACYL SYNTHASE 2.
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                                                                                                                              (Potential).
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                                                 SEQUENCE OF 3619-4427 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          493398 MW;
                              Nature 390:249-256(1997).
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                                                            STRAIN=168 / PB1424;
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DOMAIN 211 2
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                  subtilis.
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RX STAINS-912,

RA MEDLINE=21848401; PubMed=11859360;

RA WOOd V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Squercs J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

Brooks K., Brown D., Brown S., Chillingwucht T., Churcher C.M.,

Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA James K., O'Neil S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Money P., Moule S., Mungall S., Pauchers R., Squares S.,

RA Skelton J., Simmonde M., Squares R., Squares S.,

RA Skelton J., Simmonde M., Squares R., Squares S.,

RA Taylor K., Taylor R.G., Aert R., Robben J., Grymonprez B.,

RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

RA Galbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Gallbert R., Aviang Z., Hunt C., Moore K., Hurst S.M.,

RA Daga R.R., Cruzado L., Jümenez J., Sanchez M., Gelzen M., Torsburg S.L.,

RA Daga R.R., Cruzado L., Jümenez J., Sanchez M., Gelzen M., Torsburg S.L.,

RA Daga R.R., Cruzado L., Jümenez J., Sanchez M., Gelzen M., Shabkovski G.V., Ussery D., Barrell B.G., Nurse P.;

RA Shpkovski G.V., Ussery D., Barrell B.G., Nurse P.;

RI "The genome sequence of Schizosaccharomyces pombe.";

RI Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in normal nuclear morphology and chromosome stability, interacts with Dis3, Piml/RCC1 and an essential nucleoporin.", J. Cell Sci. 115:4375-4385(2002).

-!- SUBUNIT: Monomer. Interacts with ned1.

-!- SUBCELLULAR LOCATION: Nuclear pore complex (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDENTIFICATION, AND SUBUNIT.
MEDLINE-22263608; PubMed-12376568;
Tange Y., Hirata A., Niwa O.;
"An evolutionarily conserved fission yeast protein, Ned1, implicated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yoshioka S., Kato K., Nakai K., Okayama H., Nojima H.;
"Identification of open reading frames in Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Belongs to the GLFG family of nucleoporins.
                                                                                                                                                                         Bukaryota, Fungi, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae,
                Q9UTR4; P78796;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Nucleoporin nupl89 (Nuclear pore protein nupl89).
                                                                                                                                                  Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN: Contains G-L-F-G repeats.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1428-1778 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Res. 4:363-369(1997).
                                                                                                                                                                                                                   Schizosaccharomyces.
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=PR745;
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EMBL; AL133357; CAB62415.1; -. EMBL; D89145; BAA13807.1; -.

0

Gaps

·.

Length 4427;

76.1%; 62.5%;

5; Conservative

Best Local Similarity

Query Match

1205 CNEEGQVC 1212

RESULT 10 N189_SCHPO

1 CNEESLIC 8

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epoxygenase).
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INIT MET
METAL
SEQUENCE
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CPJ3_RAT
                                                                                                                                                                                            Matches
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A Kithta Y., Sogawa K., Haniu M., Kinosaki M., Kusunose E., Nojima Y.,

A Kithta Y., Sogawa K., Haniu M., Kinosaki M., Kusunose E., Nojima Y.,

A Yamamoto S., Ichihara K., Kusunose M., Pujii-Kuriyama Y.;

I chihara K., Kusunose H., Rusiii K., Pujii-Kuriyama Y.;

I chihara K., Kusunose M., Rusiii K., Pujii-Kuriyama Y.;

I chihara M., Kusunose M., Rusiii K., Pujii M., Rusiii K., Pujii M., Pujiii M., Pujii M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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HRSP; POUT99; LTG.

InterPro: IPR001128; Cytochrome P450.

InterPro: IPR008071; EP450_CYP2J.

PREM: PR00067; P450; 1.

PRINTS; PR01688; EP450ICYP2J.

PRINTS; PR01688; EP450ICYP2J.

PROSITE; P800086; CYTOCHROME P450; 1.

CX:doreductase; Monooxygenase; Blectron transport; Membrane; Heme; Microsome; Endoplasmic reticulum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryctolagus cuniculus (Rabbit).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 72.7%; Pred. No. 84;
Matches 8; Conservative 0; Mismatches 0; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                  189575 MW; 1D2AED57D927ADC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cytochrome P450 2J1 (EC 1.14.14.1) (CYPIIJ1) (P-450IB).
         PIR; TSUU, 1, 18F.
HSSP; P22629; ISWF.
GG=0B_SPOMDe; SPAC1486.05; -.
A GO:0016020; C:membrane; ISS.
R GO; GO:0005643; C:muclear pore; ISS.
NR GO; GO:0006606; P:protein-nucleus import; ISS.
NR InterPro; IPR004325; Nucleoporing.
DR Pfan; PP04095; Nucleoporing. FG.
DR Pfan; PP03093; Nucleoporing. 73.
Nuclear protein; Transport; Repeat.
KW Nuclear protein; Transport; Repeat.
Seaf. THE-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                        393 44
1778 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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P52786;
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CPJ1_RABIT
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MEDLINE=98234557; PubMed=9570962;
Ma J., Ramachandran S., Fiedorek P.T. Jr., Zeldin D.C.;
"Mapping of the CYP2J cytochrome P450 genes to human chromosome 1 and
0 0 444 446 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
500 AA; 57194 MW; AOEEBG28ESFF23DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomics 49:152-155(1998).
-!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH + oxidized flavoprotein + H(2)O.
-!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
-!- SUBLIBARITY: Belongs to the cytochrome P450 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cytochrome P450 2J6 (EC 1.14.14.1) (CYPIIJ6) (Arachidonic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.9%; Score 34; DB 1; Length 501; 85.7%; Pred. No. 28; ive 1; Mismatches 0; Indels
                                                                                73.9%; Score 34; DB 1; Length 500; 85.7%; Pred. No. 28; 0; Indels ative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                           501 AA
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |||:|||
296 NEENLIC 302
                                                                                                                                                                                                                      296 NEENLIC 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 NEESLIC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mouse chromosome 4.
                                                                                                                                                                                        2 NEESLIC 8
                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRAIN=Fischer 344;

AN MEDLINE=97284730; PubMed=9139707;

AN WEDLINE=97284730; PubMed=9139707;

AN WILD'R E., Gabel S., Tomer K.B., Foley J.,

RA Steenbergen C., Falck J.R., Moomaw C.R., Zeldin D.C.;

RI "Molecular cloning, expression, and functional significance of a strochrome P450 highly expressed in rat heart myocytes.";

RI "Molecular cloning, expressed in rat heart myocytes.";

RI "ADI. Chem. 272:12551-12559(1997).

CC "I- FUNCTION: THIS ENZYME METABOLIZES ARACHIDONIC ACID PREDOMINANTLY CC AND 9, 9-EPOXYEICOSATRIENDIC ACIDS (EET). IT ALGO ACIS AS AN OMEGA-CT AND 9, 9-EPOXYEICOSATRIENDIC ACID (19-OH-AA).

CC "I- HYDROXYLASE BY METABOLIZING ARACHIDONIC ACID TO 19-CATALYTIC ACITUTY: RH + reduced flavoprotein + 0(2) = ROH + coxidized flavoprotein + H120.

CC "I- SUBCELIULAR LOCATION: Membrane-bound. Endoplasmic reticulum.

CC "I ISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN HEART AND LIVER.

CC "I- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN HEART AND LIVER.

CC "I- SIMILARITY: Belongs to the cytochrome P450 family.
                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HEME AXIAL LIGAND) (BY SIMILARITY).
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PROSITE; PS00086; CYTOCHROME P450; 1.
Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leucine-rich repeat LGI family member 2 precursor (Leucine-rich
glioma-inactivated protein 2) (LGII-like protein 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCOAE67977FFF31 CRC64;
                                                                     01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cytochrome P450 2J3 (EC 1.14.14.1) (CYPIIJ3).
                  502 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Microsome; Endoplasmic reticulum; NADP.
METAL 448 448 TPON (HEME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001128; Cytochrome P450.
InterPro; IPR008071; EP450_CYP23.
Pfam; PF00067; p450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IRON
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HSSP; P00179; 1DT6.
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Homo sapiens (Human).
           STANDARD;
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297 NEENLIC 303
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
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LG12 HUMAN
LD 14012 HUMAN
LD 10-0CT-
DT 10-0CT-
DE Leucin
DE Leucin
DE Glioma-
GN LG12 Of
GN CEUCHT
NAME OF THE PROPERTY OF THE PR
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                            Gu W., Wevers A., Schroder H., Grzeschik K.H., Derst C., Brodtkorb E., de Vos R., Steinlein O.K., "The LGII gene involved in lateral temporal lobe epilepsy belongs to a new subfamily of leucine-rich repeat proteins."; FEBS Lett. 519:71-76(2002).
                                                                                                                                                                                                                                                                       "The novel EPTP repeat defines a superfamily of proteins implicated in epileptic disorders.";
Trends Blochem. Sci. 27:441-444(2002).
                                                                                                                                                                                                                                                                                                                                                              Nagase T., Kikuno R., Ohara O., "Prediction of the coding sequences of unidentified human genes. XXI. The complete sequences of 60 new cDNA clones from brain which code for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEUCINE-RICH REPEAT LGI FAMILY MEMBER 2.
                                                                                                                                               MEDLINE=22090568; PubMed=12085917;
Scheel H., Tomiuk S., Hofmann K.;
"A common protein interaction domain links two recently identified
                                                                                                                                                                                                                                    MEDLINE=22207944; PubMed=12217514;
Staub E., Perez-Tur J., Siebert R., Nobile C., Moschonas N.K.,
Deloukas P., Hinzmann B.;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Contains 5 EAR repeats.
-!- SIMILARITY: Contains 4 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                              NA_Res. 8:179-187(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                      epilepsy genes.";
Hum. Mol. Genet. 11:1757-1762(2002).
                                                 MEDLINE=22017856; PubMed=12023020;
                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21456161; PubMed=11572484;
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LRR
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EAR
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EMBL, AJ487958, CAD32305.1; --
EMBL, AJ487516; CAD31784.1; --
EMBL, AB067503; BAB67809.1; --
                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 4-545 FROM N.A.
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InterPro; IPR009039; EAR.
                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                    SEQUENCE FROM N.A.
              NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                     large proteins."
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22207944; PubMed=12217514;
Staub E., Perez-Tur J., Siebert R., Nobile C., Moschonas N.K.,
Deloukas P., Hinzmann B.;
"The novel BPTP repeat defines a superfamily of proteins implicated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
  EAR 5.
N-LINKED (GLCNAC. . .) (POTENTIAL).
F -> L (IN REF. 2 AND 4).
M, FD29B51F01B3D7E2 CRC64;
                                                                                                                                                                                                                        08K4Z0; 080T76;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last mnotation update)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Created)
                                                                                                                 ;
                                                                                        Score 34; DB 1; Length 545;
Pred. No. 31;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISOId-09K4Z0-2; Sequence=VSP 007680, VSP_007681; -!- SIMILARITY: Contains 5 EAR repeats. -!- SIMILARITY: Contains 4 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                    550 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                    epileptic disorders.";
Trends Biochem. Sci. 27:441-444(2002).
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EMBL; AK122570; BAC65852.1; ALT_INIT.
MGD; MGI:2180196; Lgi2.
InterPro; IPR009039; EAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1).
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                                                                      62298 MW;
                                                                                           73.9%;
62.5%;
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70 186 1
271 2
402 4
524 5
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Best Local Similarity
Matches 5; Conserv
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CARBOHYD
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LGI2_MOUSE
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LEUCINE-RICH REPEAT LGI FAMILY MEMBER 2.
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N-LINKED (GLCNAC. .) (POTENTIAL)
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                                                                                                                                                                                                                                                                               Signal; Alternative splicing.
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/FTId=VSP 007681.
56974B9DE663CCD1 CRC64;
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Best Local Similarity 62..
Si Conservative
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InterPro; IPR005492;
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5, 2004, 09:46:09; Search time 18.101 Seconds (without alignments) 139.448 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		Oglaba rattus gair		Collect Land	Operate Dactilus an	Correct mirch			Cante capreolus c	Quant capra hircu	Q9mzbl ovis aries	Q866g4 oryctolagus	O9n1s1 capreolus c	OBmiles Agrando	OSTITED SECTION	Usymis ori virus.	Q80ge8 orf virus.	042571 xenopus lae
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ALIGNMENTS

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RA Diaz-Trelles R., Radriguez-Leon J., Kawakami Y.,

RA Diaz-Trelles R., Rodriguez-Leon J., Kawakami Y.,

RA Izpisua-Belmonte J.C.;

RT "Expression of the chick vascular endothelial growth factor D gene during limb development.";

RE MEME, AR479650; ARM12733.1;

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:000813; F:growth factor activity; IEA.

DR GO; GO:000813; F:growth factor activity; IEA.

DR GO; GO:000813; P:eell growth and/or maintenance; IEA.

DR ProDom; PD001629; PD_growth_factor.

DR ProDom; PD001629; PD_growth_factor; 1.

DR SMART; PS00249; PDGFF 1; 1.

DR PROSITE; PS00249; PDGFF 1; 1.

DR PROSITE; PS0278; PDGFF 1; 1.

SGUIENCE 252 AA; 28767 MW; 643475DAB2E72F27 CRC64;
                                            080507;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2003 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBL)
Vascular endothelial growth factor D.
Gallus gallus (Chicken)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianiaee;
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87.5%; Pred. No. 1.8;
ive 0; Mismatches 1; Indels
                                       252 AA.
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                                 PRELIMINARY;
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                                 Q8QGD7
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RESULT 1
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OY 1 CNESLIC 8
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Kirkin V., Mazitschek R., Krishnan J., Steffen A., Waltenberger J.,

Rirkin V., Mazitschek R., Sleeman J.P.;

Rirkin V., Mazitschen G. Sleeman J.P.;

Rirkin V., Blochem O. 0:0-0'2001.

R. Characterization of UNGORN-3 but not UNGFR-2.";

R. Characterization of UNGORN-3 but not UNGFR-2.";

R. Characterization of UNGORN-3 but not UNGFR-2.";

R. Characterization of UNGFR-3 but not UNGFR-2.";

R. Characterization of UNGFR-3. I.

R. Characterization of UNGFR-3. I.

R. Characterization of UNGFR-3. I.

SMART: SMO0141; POGF: 1.

SR PROSITE; PSSO0249; PDGF-1: I.

SR PROSITE; PSSO0249; PDGF-2: I.
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                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Parapoxvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          with A property of the control of th
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Wascular endothelial growth factor-like protein.
                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152 AA
                                                                                                                                                                                      326 AA
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                                                                                                                                                                                          PRELIMINARY;
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Best Local Similarity
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                                                                                                                                                                                          Q91ZE4
Q91ZE4;
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Read T.D., Peterson S.M., Tourasse N., Baillie L.W., Paulsen I.T., Read T.D., Peterson S.M., Tourasse N., Bisen J.A., Gill S.R., Melson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R., Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M., Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M., Relson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.H., Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman W.C., Berry K.J., Plaut R.D., Wolf A.M., Warkins K.L., Nierman W.C., Barry K.J., Plaut R.D., Wolf A.M., Warkins K.L., Nierman W.C., Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Capra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The genome sequence of Bacillus anthracis Ames and comparison to closely related bacteria.";
Nature 423:81-86(2003).
BEMB.; AB01040; AAP28871.1; -.
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                                                                                                                       80.4%; Score 37; DB 12; Length 152; 75.0%; Pred. No. 4.9;
                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus anthracis (strain Ames).
Bacteria, Firmicutes, Bacillales; Bacillaceae, Bacillus.
NCBI_TaxID=198094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 protein; Complete proteome.
200 AA; 23905 MW; 70E8DD90E5DBA7A0 CRC64;
                                                    550278; PDGF 2; 1.
152 AA; 16202 MW; F4B3956D60B37A3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Vascular endothelial growth factor 121 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                     OBIXNI;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 A.A.
                                                                                                                                                                                 1; Mismatches
Prodom; PD001629; PD_growth_factor; 1.
SMART; SM00141; PDGF; 1.
PROSITE; PS50278; PDGF_2; 1.
SEQUENCE 152 AA; 16202 MW; F4B3956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                      6; Conservative
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TISSUE=Corpus luteum;
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                                                                                                                                       Query Match
Best Local Similarity
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SEQUENCE 20
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Skorjanc D., Jaschinski F., Heine G., Pette D.;
"Sequential increases in capillarization and mitochondrial enzymes in low-frequency-stimulated rabbit muscle.",
Am. J. Physiol. 274:C810-C818(1998).
EMBL; AF022179; AAC15469.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Capreolus capreolus (Roe deer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
Cervidae; Odocoileinae; Capreolus.
                                                                                                                                                                     Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wagener A., Blottner S., Goritz F., Fickel J., "Detection of growth factors in the testis of roe deer (Capreolus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Vascular endothelial growth factor isoform 121 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.3%; Score 36; DB 6; Length 75; 75.0%; Pred. No. 4.1; 75.0%; Ive 1; Mismatches 1; Indels
                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; But
Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GG; GG:0016020; C:membrane; IEA.
GG; GG:0008083; F:growth factor activity; IEA.
GG; GG:0008083; F:growth factor activity; IEA.
GG; GG:0008081; F:growth and/or maintenance; IEA.
InterPro; IPR002400; GF cysknot.
InterPro; IPR002000; GF cysknot.
FRAM: PR0041; PDGF; 1.
ProDom; PR00438; GFCYSKNOT.
ProDom; PR001629; PD growth factor; 1.
SMART; SM00141; PDGF; 1.
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GO; GO:0008083; F:growth factor activity; IEA.
GO; GO:00080151; P:cell growth and/or maintenance; IEA.
InterPro; IPR002400; GF cysknot.
InterPro; IPR000072; PD_growth_factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 AA; 8720 MW; DDCE2C5B29E69359 CRC64;
                         01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Vascular endothelial growth factor (Fragment).
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=NBW ZEALAND WHITE; TISSUE=Skeletal muscle;
MEDLINE=98191144; PubMed=9530113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Testis;
MEDLINE=20532861; PubMed=11078967;
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Anim. Reprod. Sci. 64:65-75(2000).
EMBL; AF152599; AAF73232.1;
HSSP; P49763; 1FZV.
                                                                                                                                      Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00249; PDGF 1; 1.
PROSITE; PS50278; PDGF 2; 1.
NON_TER 1 1 1 NON_TER 75 75
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PRINTS; PR00438; GFCYSKNOT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
6; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29 CNDESLEC 36
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                                                                                                                                                                                                                        NCBI_TaxID=9986;
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Q9N1S2;
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                         PACOCCOS ON THE STATE OF THE ST
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Kawate N., Tsuji M., Tamada H., Inaba T., Sawada T.;

"Changes of Messenger RNAs Encoding Vascular Endothelial Growth Factor and Its Receptors during the Development and Maintenance of Caprine Corpora Lutea.";

Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

RDBL, AY114353; ARM76674.1;

RO; GO:001620; C:membrane; IEA.

GO; GO:001620; C:membrane; IEA.

GO; GO:001620; P:cell growth factor activity; IEA.

RO; GO:0008151; P:cell growth and/or maintenance; IEA.

RINTERPRO; IPR000072; PD_growth_factor.

REM: PF00341; PDGF; 1.

REM: PF00341; PDGF; 1.

REM: PROSITE; PS50278; PDGF; 1.
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Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 6; Length 65; Pred. No. 3.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Inoue K., Kawabe Y., Kodama T.;
"Rabbit VRGF cDNA, partial.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB020215; BAA36949.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO: 0016020; C: membrane; IEA.
GO; GO: 00080813; F: growth factor activity; IEA.
GO; GO: 0008151; P: cell growth and/or maintenance; IEA.
InterPro; IPR000072; PD_growth_factor.
Pfam, PR00341; PDGF; 1.
ProDom: PD001629; PD_growth_factor.
SMART; SM00141; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                     65 AA; 7562 MW; BA3E5384364B05E3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-UIN-2003 (TrEMBLrel. 24, Last annotation update)
Vascular endothelial growth factor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.3%; Score 36; DB 6; 75.0%; Pred. No. 3.8; tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.3%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00249; PDGF 1; 1. PROSITE; PS50278; PDGF 2; 1.
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Best Local Similarity 75.v.,
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Best Local Similarity 75.v.
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58 CNDESLEC 65
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TISSUE-Corpus luteum;
TRANTE N., TSUJI M., Tamada H., Inaba T., Sawada T.;
Kawate N., TSUJI M., Tamada H., Inaba T., Sawada T.;
and Tespros of Messenger RNAs Encoding Vascular Endothelial Growth Factor and Its Receptors during the Development and Maintenance of Caprine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Bukaryota: Metazooa; Chordata; Craniata; Vertebrata; Euteleostomi;
Rammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0072-2002 (TrEMBLrel. 22, Created)
01-0072-2002 (TrEMBLrel. 24, Last sequence update)
01-0072-2003 (TrEMBLrel. 24, Last sequence update)
01-010N-2003 (TrEMBLrel. 24, Last annotation update)
Vascular endochelila growth factor 165 (Fragment).
Capra hircus (Goat).
Capra hircus (Goat).
Mammalia, Metacoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia, Eutheria, Cetartiodactyla; Ruminantia, Pecora; Bovoidea;
Bovidae; Caprinae, Capra.
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                                                                                                                                                                            78.3%; Score 36; DB 6; Length 78; 75.0%; Pred. No. 4.3; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corpora Lucted (NAY-2002) to the EMBL/GenBank/DDBJ databases. Submitted (NAY-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AY114455. Sol. 60. 60.0016020; C:membrane; IEA. 60. 60.0016020; C:membrane; IEA. 60. 60.0016020; F:growth factor activity; IEA. Interpro; IPRO0072; PD_growth and/or maintenance; IEA. Interpro; IPRO00072; PD_growth_factor. ProDom; PD001629; PD_growth_factor. Brobom; PD001629; PD_growth_factor. SWART; SW00141; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQÜENCE 109 AA; 12656 MW; 912657251A37E023 CRC64;
                                                                                                                                     78 AA; 9131 MW; 7EE20DDFFC17847C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Vascular endothelial growth factor (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                           109 AA.
      PD001629; PD_growth_factor; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50278; PDGF2; 1.
                         SMART; SM00141; PDGF; 1.
PROSITE; PS00249; PDGF 1; 1.
PROSITE; PS50278; PDGF 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
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                                                                                                                                                                                                                              6; Conservative
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Best Local Similarity
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Best Local Similarity
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SEQUENCE
         ProDom;
SMART; S
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Q8MIN1
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SEQUENCE FROM N.A.
TISSUB-Placental artery endothelium;
TISSUB-Placental artery endothelium;
TISSUB-Placental artery endothelium;
Zheng J., Tsoi S.C., Magness R.R.;
Growth factor expression in ovine fetal placental artery endothelial
cells.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AR250375; AAR75258.1;
HSSP; P49763; IFZV.
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Transcriptional changes in rabbit preimplantation blastocysts upon exposure to polychlorinated biphenyls.";
submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY196796; AAO42518.1; ---
GO; GO:0008083; Fignowth factor activity; IEA.
GO; GO:0008083; Fignowth factor activity; IEA.
InterPro; IPR002400; GF_Cysknot.
InterPro; IPR002040; GF_Cysknot.
InterPro; IPR002040; GP_Cysknot.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Lagomorpha, Leporidae, Oryctolagus.
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Local Similarity 75.0%; Pred. No. 6.3;
local Conservative 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQÜENCE 118 AA; 13931 MW; 757DC53AA56378A6 CRC64;
                                                                                                                                                                                                                                                               GO; GO:0016020; C:membrane; IEA.
GO; GO:0008083; F:growth factor activity; IEA.
GO; GO:0008151; P:cell growth and/or maintenance; IEA.
InterPro; IPR0002400; GF_cysknot.
InterPro; IPR00072; PD_growth_factor.
InterPro; PR000172; PD_growth_factor.
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01-UTN-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Vascular endothelial growth factor (Pragment).
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PRINTS; PR00438; GFCYSKNOT.
ProDom; P001629; PD growth_factor; 1.
SMART; SM00141; PDGF; 1.
PROSITE; PS00249; PDGF 1; 1.
PROSITE; PS50278; PDGF 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                Print Production Programmer, SMART; SMOO141; PDGF; 1.

PROSITE; PSCO278; PDGF 1; 1.

PROSITE; PSCO278; PDGF 2; 1.
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Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Cervoidea,
Cervidae, Odocoileinae, Capreolus.
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Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Cervoidea,
Cervidae, Odocolleinae, Capreolus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wagener A., Blottner S., Goritz F., Fickel J., "Detection of growth factors in the testis of roe deer (Capreolus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :0
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Vascular endothelial growth factor isoform 165 (Fragment)
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0008151; P:cell growth and/or maintenance; IEA.
InterPro; IPR002400; GF_cysknot.
InterPro; IPR00341; PDGF; 1.
Pfam; PF00341; PDGF; 1.
ProDom; PD001629; PD growth_factor.
ProDom; PD001629; PD growth_factor; 1.
SMART; SM00141; PDGF; 1.
PROSITE; PS00249; PDGF; 1.
NOW THE.
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"Detection of VBGF in roe deer testis.";
"Detection of WBGF in roe deer testis.";
Submitted (MAX-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF514284 AM449789.1;
GO; GO:0016020; C:membrane; IEA.
GO; GO:0008083; F:growth factor activity; IEA.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Vascular endothelial growth factor-3 (Fragment)
Capreolus capreolus (Roe deer)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.3%; Score 36; DB 6; 75.0%; Pred. No. 6.6; Live 1; Mismatches
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                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20532861; PubMed=11078967;
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                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                               PRELIMINARY;
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74 CNDESLEC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 CNDESLEC 32
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Matches 6, Conserv
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TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9858;
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                                                                               RESULT 12
O901S1
ID 0901S1
ID 01-OC
DT 01-OC
DT 01-UU
DB VASCU
GB VASCU
CC CUKAT
OC CAPTE
OC 
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Debio C., Buttner M.;
The latedheess and heterogeneity at the near-terminal end of the genome of a parapoxvirus bovis 1 strain (B177) compared with parapoxvirus ovis (Orf virus).;
J. Gen. Virol. 84:111-1116(2003).
REMBL; AR106720; AAD03735.1;
REMBL; AR106720; AAD03735.1;
REMBL; AR106720; AAD03735.1;
REMBL; AR106720; AAD03735.1;
REMBL; AR106720; AAD03702.1;
REMBL; AR106720; Cimembrane; IEA.
GO; GO:0008131; P:cell growth factor activity; IEA.
RO; GO:0008151; P:cell growth and/or maintenance; IEA.
RICEPRO; IRR002400; GF Cysknot.
RICEPRO; IRR002400; GF Cysknot.
RICEPRO; REMORA REMORA REMORA REMORAL 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Meyer M., Clauss M., Lepple-Wienhues A., Waltenberger J., Augustin H.G., Ziche M., Lanz C., Buettner M., Rziha H.J., Dehio C.; "A novel vascular endothelial growth factor encoded by orf virus, VEGF-E, mediates anglogenesis via signalling through VEGFR-2 (KDR) but EMBO J. 18:363-374(1999).
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Orf virus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Parapoxvirus.
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01-MAY'1999 (TrEMBLrel. 10, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last amnotation update)
Vascular endothalial growth factor homolog Vegf-e (Vascular endothelial growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 78.3%; Score 36; DB 12; Length 132; Best Local Similarity 75.0%; Pred. No. 7; Matches 6; Conservative 1; Mismatches 1: Tindel.
                                                                                                                                                                                                                                                                    78.3%; Score 36; DB 6; Length 131; 75.0%; Pred. No. 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
GO; GO:0008151; P:cell growth and/or maintenance; IEA. InterPro; IPR000072; PD growth_factor. Prom; PF00341; PDGF; I. the ProDom; PD001629; PD growth_factor; 1. SMART; SM00141; PDGF; 1. PROSITE; PS50278; PDGF; 2; 1.
                                                                                                                                                                                                                  131 AA; 15358 MW; 99719A58EEAC7FCA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEAM; PR00341; PDGF; 1.
PRINTS; PR00438; GFCYSKNOT.
ProDom; PD001629; PD growth factor; 1.
SMART; SM00141; PDGF; 1.
PROSITE; PS00249; PDGF 1; 1.
PROSITE; PS50278; PDGF 2; 1.
SEQUENCE 132 AA; 14763 MW; 15F403A068B72926 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 AA
                                                                                                                                                                                                                                                                                                                            1; Mismatches
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                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                3 CNDESLEC 10
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                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10258;
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                                                                                                                                                                                                             SEQUENCE
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NON TER
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STRAIN-Orf-11;

A McInnary Lanscript map of the early genes of orf virus.";

A preliminary transcript map of the early genes of orf virus.";

Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

EMBL A2236120; AAR03726.1;

CO, GO:00016020; C:membrane; IEA.

GO; GO:0008131; F:erl growth factor activity; IEA.

GO; GO:0008131; F:erl growth and/or maintenance; IEA.

InterPro; IPR002400; GF_cysknot.

R GO; GO:000813; PR00403; PD_growth_factor.

PROBORY: SMO0439; GFCXSKOT.

PROBOM; PR00141; PDGF; 1.

PROBORY: SMO0441; PDGF; 1.

PROSITE; PS00249; PDGF; 1.

PROSITE; PS00249; PDGF; 1.

PROSITE; PS00249; PDGF_1; 1.

PROSITE; PS00249; PDGF_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses, dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Parapoxvirus.
NCBI_TaxID=10258;
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Best Local Similarity 75.0%; Pred. No. 7.2;
Matches 6; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                             01-JUN 2003 (TrEMBLrel. 24, Created) 01-JUN 2003 (TrEMBLrel. 24, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) VEGF-like protein.
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                                                   70 CNDESLEC 77
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1 CNEESLIC 8
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AC Q80GE8
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Search completed: September 5, 2004, 09:59:54 Job time : 20.101 secs

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Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2004
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protein search, using sw model 1 OM protein

2004, 09:37:49; Search time 26.2626 Seconds (without alignments) 86.068 Million cell updates/sec ς, September Run on:

US-09-761-636A-6 Title: Perfect

CNEESLIC 8 score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

1586107 seqs, 282547505 residues Searched:

of hits satisfying chosen parameters: Total number

seq length: 0 seq length: 200000000 Minimum DB s Maximum DB s

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq 29Jan04:* Database :

geneseqp2001s:*
geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2004s:* W.4. N.0. L. B

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	F	11			Q.	Human VEG	Human VEG	Human vas	Human tru	Human wil	Human NVR		Human VEG	Human vas	Human zve	Homo sapi	Human VEG	Human pre			Human VEG	Human VEG	Polypepti	Human vas	Human Flt		Himan VEC		
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VEGF base VEGF base	Human VEG VEGF base Rat vacou	VEGF base Human vas	Human c-F Novel hum	Poxvirus Poxvirus	Mouse VEG Poxvirus Poxvirus	Bovine va Bovine VE	Parapox v Parapox v Orf virus
Aau04541 Aau04538 Aau04552	Aau04553 Aaw44296	Aau04540 Aab70685	Aaw14994 Abg20904	Aaw86229 Aaw86228	Aam4 /933 Aaw86227 Aaw86226	Aar10916 Aar38916	Aaw40305 Aay33434 Aay92776
AAU04541 AAU04538 AAU04552 ABG73750	AAU04553 AAW44296	AAU04540 AAB70685	ABG20904	AAW86228 AAM47933	AAW86227 AAW86226	AAR10916 AAR38916	AAY33434 AAY32776
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26 27 28 29	30 31	2 E E	35 36	37 38	w 4 4	1 4 4 1 2 E	<u>4. 4.</u> ር

ALIGNMENTS

AAU04525 standard; peptide; 8 AA. VEGF based monocyclic peptide 2. (first entry) 26-SEP-2001 AAU04525;

Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.

Synthetic.

1. .8 /note= "This bond cyclises the peptide" Location/Qualifiers Disulfide-bond WO200152875-A1 26-JUL-2001.

18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P. 18-JAN-2001; 2001WO-US001533.

(LUDW-) LUDWIG INST CANCER RES.

Cendron A; Stacker S, Achen MG, Hughes RA,

WPI; 2001-442248/47

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine

Claim 49; Page 32; 102pp; English.

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human vEGFD (vascular endothelial growth factor). The invention relates to method of producing a monomeric monocyclic peptide by a measuring betabeta carbon separation distances on opposite antiparallel strands of a

WPI; 2001-442248/47.

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peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptides by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis.

CC to cyclisation are used to interfere with angiogenesis.

CC haracterised by angiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis.

CC The condition is diabetic retinopathy, psoriasis, arthropathy, cerebrovascular accident, post-angioplasty restenosis, head, heat or cold crauma, substance-induced neovascularisation of the liver, excessive crauma, substance-induced neovascular sequelae, hypertension induced neovascular sequelae, nor chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to inage blood vessels and lymphatic or brain. The mentioneric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF. VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a signal control or inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _note= "A disulfide bond forms between residue 1 and residue 1 of an identical peptide to form a dimeric peptide, or between residue 1 and residue 17 of the sequence appearing as AAU04527 also forming a dimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphanglogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 46; DB 4; Length 8; 100.0%; Pred. No. 1.4e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEGF based bicyclic dimeric peptide #2.
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16-MAY-2000; 2000US-0204590P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                             diabetic retinopathy
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Best Local Similarity
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Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8 AA;
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Achen MG,

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Gaps 0;

Indels

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The sequence represents a dimeric bicyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human vEGFD (vascular endothelial growth factor). The invention relates to a vEGFD (vascular endothelial growth factor). The invention relates to a vEGFD (vascular endothelial growth factor). The invention relates to a beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptides (comprising 2 linked monocyclic cyclisation are used to interfere with angiogenesis, a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis.

The condition is diabetic retinopathy, psoriasis, arthropathy.

The condition is diabetic retinopathy, psoriasis, nead, heat or cold creebrovascular accident, post-angioplasty restenosis, head, heat or cold creebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive controne-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver correctives of the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, corrective the mammal has a condition characterised by fluid arcumulation in peripheral limbs or in lungs, being being and lymphalic corrective and bicyclic peptides are used to incede are used to incede are used to incede and bicyclic peptides are used to incede are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially returned arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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                                           Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; VEGF-D; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphanglogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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100.0%; Pred. No. 1.4e+06;
ive 0: Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human VEGF-D amino acids Val101-Thr 173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU04522 standard; protein; 73 AA.
                                                                                                                                                                     Claim 59; Page 32; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-JAN-2001; 2001WO-US001533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JAN-2000; 2000US-0176293P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200152875-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU04522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                      residues.
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The sequence represents Human VEGF-D (vascular endothelial growth factor)

CC amino acids Val101-Thr 173, used together with the C-terminal 23 residues

CC of VEGF to make a hybrid theoretical molecule for 3 dimensional

modelling. The sequence is used in a method of producing a monomeric

CC moposite antiparallel strands of a peptide loop fragment from an

CC oxidising the cysteine residues. The monocyclic peptides dimeric

CC oxidising the cysteine residues. The monocyclic peptides dimeric

CC oxidising the cysteine residues. The monocyclic peptides dimeric

CC oxidising the cysteine residues. The monocyclic peptides and a cyclic

CC oxidising the cysteine residues. The monocyclic peptides and a cyclic

CC oxidising the cysteine residues. The monocyclic peptides and a cyclic

CC oxidising the cysteine residues. The monocyclic peptides and a cyclic

CC oxidising the cysteine residues. The monocyclic peptides and a cyclic

CC used to interfere with angioenesis, neovascularisation or lymphangiogenesis. The condition is

CC used to interfere with peptides are also

CC diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised

CC diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised

CC diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised

CC dysfunction, diabetes induced neovascular sequelae, hypertension induced

CC dysfunction, diabetes induced neovascular sequelae, hypertension induced

CC dysfunction, diabetes induced neovascular sequelae, hypertension induced

CC dysfunction characterised by fluid accumulation in peripheral limbs or in

CL lungs, peritoneal cavity, pleura, or brain. The peptides are used to

CC madge blood vessels and lymphatic vasculature. The monomeric and bicyclic

CC medical by VEGF, VEGF- Or -D and are also used in combination with an interferent and indial artivity

Anti-inflammarry, anone to read a second in combination with anti-inflammarry.
                                                                                                                                                                                                                             Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy
                                                                                                                         Cendron A;
                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 90-91; 102pp; English
                                                                                                                      Stacker S,
                                                      (LUDW-) LUDWIG INST CANCER RES.
   16-MAY-2000; 2000US-0204590P.
                                                                                                                   Hughes RA,
                                                                                                                                                                         WPI; 2001-442248/47.
                                                                                                                Achen MG,
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Sequence 73 AA;

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             100.0%; Score 46; DB 4; Length 73; 100.0%; Pred. No. 1.1; ative 0; Mismatches 0; Indels
                        1.1;
hes 0; Indels
Ouery Match
Best Local Similarity 100...
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CNEESLIC 53 1 CNEESLIC 8 46 셤

AAU04520 standard; protein; 96 AA. AAU04520;

26-SEP-2001 (first entry)

Human VEGF-D amino acids Val101-PRO186.

Human; VEGF-D; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation.

Homo sapiens

WO200152875-A1.

26-JUL-2001.

18-JAN-2001; 2001WO-US001533.

18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P.

(LUDW-) LUDWIG INST CANCER RES

Cendron A; Stacker S, Achen MG, Hughes RA,

WPI; 2001-442248/47.

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues

Example 1; Page 89; 102pp; English.

The sequence represents Human VEGF-D (vascular endothelial growth factor)

a mino acids Val101-PR0186. The sequence is used in a method of producing camino acids Val101-PR0186. The sequence is used in a method of producing distances on opposite antiparallel strands of a peptide loop fragment confirm an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric by oxidising the cysteine residues. The monocyclic peptides dimeric confirming a linked monocyclic peptides, dimeric peptide with at least one amino acid deleted prior to cyclisation are consecuted to interfere with angiogenesis. The condition are lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy psoriasis, arthropathy, hemangioma, vascularised condition is manignant or benign tumour, post-recovery cerebrovascular accident, post-recovery carebrovascular accident, post-recovery carebrovascular accident, post-neovascular sequelae, or chronic liver infection. The peptides are also condition characterised by fluid accommunial has a condition characterised by fluid accumulation in peripheral limbs or in climage blood vessels and lymphanic vasculature. The monomeric and bicyclic condition characterises with a past one bicker one in specifies are used to media the maning and picyclic condition characterise with a place of the maning and picyclic condition characterise with a place of the maning and picyclic condition characterise with a place of the maning and picyclic condition characterise with a place of the maning and picyclic condition characterise with a place of the maning and picyclic conditions and picyclic condition characterise with a place of the page of the maning and picyclic condition characterise with a place when the page of the place when the page of the maning and picyclic condition characterised by fluid accumulation in peripheral limbs. peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with santi-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy

Sequence 96 AA;

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Gaps

Gaps 0; 100.0%; Score 46; DB 4; Length 96; 100.0%; Pred. No. 1.4; 0; Indels Mismatches 0 8, Conservative Local Similarity Query Match Matches

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AAY23889 standard; protein; 109 AA. RESULT 5 AAY23889

Human vascular endothelial growth factor (VEGF)-D.

(first entry)

21-SEP-1999

Vascular endothelial growth factor; VEGF; VEGF-D; malignant melanoma; tumour; psoriasis; angiogenesis; lymphangiogenesis; skin graft; wound healing; lymphedema; scleroderma; anhydrotic ectodermal dysplasia.

Homo sapiens

24-DEC-1997;

29-MAY-1998;

23-DEC-1998;

W09933485-A1

08-JUL-1999

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This sequence represents a 109 amino acid truncated human VEGF-D
(vascular endothelial growth factor D), lacking both the N- and C-
(vascular endothelial growth factor D), lacking both the N- and C-
terminal regions. The invention relates to a monoclonal antibody, or
fragments thereof, which is specifically reactive with the truncated
invention interferes with the binding of VEGF-D to the VEGF receptors
invention interferes with the binding of VEGF-D to the VEGF receptors
CVEGFR-3, but does not interfere with the binding of VEGF to
these receptors and additionally is not reactive with VEGF-C. The
antibody may be used to treat disorders associated with vascular
continuous proposesis, neovascularisation and endothelial cell
intropathies. The antibody may also be used to treat fluid accumulation
carthropathies. The antibody may also be used to treat fluid accumulation
in the heart and/or lung via modulation of vascular permeability. It may
additionally be used to detect VEGF-D and may be used to image lymphatic
                                                                                                                                                                                                                                                               Novel compositions comprising antibodies reactive to vascular endothelial growth factor-D, useful for treating, e.g. angiogenesis, lymphogiogenesis and neovascularization disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 46; DB 3; Length 109; 100.0%; Pred. No. 1.6; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB84621 standard; protein; 109 AA.
                                                                                                                                  (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 1; 44pp; English.
              99WO-US031332.
                                                             98US-0113254P.
99US-0134556P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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/note=
                                                                                                                                                                                 Achen MG, Stacker SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vasculature in tissue
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                   21-DEC-1999;
                                                                  21-DEC-1998;
                                                                                        17-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB84621;
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Matches
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%#X##X#X#X#X#X#####X#X#X##X#X#X
                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents human vascular endothelial growth factor (VEGF)-D. The specification describes a human cell line which stably expresses VEGF-D, or fragments/analogues having VEGF-D biological cativity. VEGF-D arragonists, e.g. antisense nucleic acids or triplex activity. VEGF-D arragonists, e.g. antishoses nucleic acids or triplex useful for the treatment or alleviation of malignant melanomas, tumours or useful for the treatment or alleviation of malignant melanomas, tumours or vegF-D can be administered to enhangingenesis stimulating amounts of skin grafts or to stimulate to enhance the acceptance and/or healing of skin grafts or to stimulate to enhance the acceptance and/or healing of to the skin. Lymphangiogenesis stimulating amounts of to treat lymphangiogenesis stimulating amounts of to treat suped to treat soleroderma. Vascularisation stimulating amounts of VEGF-D can be used to treat anhydrotic ectodermal dysplasia. VEGF-D corresponders are useful for detecting tumours expressing VEGF-D brulty-corresped WEGF-D can be used to stimulate at least one VEGF-D broactivity chosen from endothelial cell proliferation, migration, survival and differentiation and lymphangiogenesis without inducing vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
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                                                                                                                                                                                                                                                                                                                                                        A human cell line stably expressing vascular endothelial growth factor D, useful for treating melanomas or tumors expressing VEGF-D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB11931 standard; protein; 109 AA.
                                                                                                                                                                                                                                                                    Achen MG, Stacker SA, Alitalo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Page 72; 79pp; English.
                                                                                                                                                                                                                     LUDW-) LUDWIG INST CANCER RES
                                                                                                  98WO-US027373.
                                                                                                                                                 97AU-00001131.
98US-0087392P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-NOV-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human truncated VEGF-D
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                                                                                                                                                                                                                                                                                                                     WPI; 1999-405368/34
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Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 109 AA;
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permeability

Query Match

0

Gaps

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Human, single-chain; extracellular ligand-binding domain; VEGF;
vascular endothelial growth factor; VEGF type 2 receptor; KDR; Flt-4;
VEGF type 3 receptor; VEGF-C; VEGF-D; signal transduction; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "region of monomer likely to be modified by mutation as described in claim 9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "region of monomer likely to be modified by
mutation as described in claim 9"
                                                                                                                                                                                                                                                                                                                                                                                                      /note= "region of monomer likely to be modified by mutation as described in claim 9"
                                                         Human wild-type VEGF-D monomer SEQ ID 3.
                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
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Homo sapiens

AAB11931;

54

ò g RESULT 6 AAB11931 29-JUN-2000

"This residues is described as Gln in Claim 9"

98.

/note=

9

/note= "region of monomer likely to be modified by mutation as described in claim 9"

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Novel single-chain dimeric polypeptide for inhibiting angiogenesis, binds to extracellular ligand-binding domain of vascular endothelial growth factor type 2/type 3 receptor but does not activate the receptor.
                                                                                                                                                                                    Claim 9; Page 66; 71pp; English.
                                                                        08-APR-2002; 2002WO-DK000233
                                                                                      06-APR-2001; 2001DK-0000578
                                                                                               06-APR-2001; 2001US-0282239P
                                                                                                             (MAXY-) MAXYGEN HOLDINGS LTD.
                                                                                                                           Boesen TP, Halkier T;
                                                                                                                                          WPI; 2003-058505/05
Misc-difference
                                            WO200281520-A2
                                                          17-0CT-2002
               Region
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This invention describes a novel single-chain dimeric polypeptide which binds to extracellular ligand-binding domain of vascular endothelial cycopy that factor (VEGF) type 2 receptor (KDR) or VEGF type 3 receptor (Flt-4). The polypeptide of the invention comprises two receptor-binding sites of which one is capable of binding to a ligand-binding domain of the receptor, and at least one monomer of the dimeric domain of the receptor, and at least one monomer of the dimeric colypeptide is derived from VEGF-C or VEGF-C), where the polypeptide of cativating the receptor. The polypeptide of the invention is useful for preparing a medicament for preparing or treating or treating a disease or condition involving concreased signal transduction from, or an increased activation of a VEGF-C increased signal transduction from, or an increased activation of a VEGF-C type 2 or type 3 receptor e.g. for inhibiting anglogenesis or condition involving companies of the invention of a VEGF-D monomer which can be modified and used in the construction of a VEGF-D was a described in the disclosure of the invention
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54 CNEESLIC 61
1 CNEESLIC 8
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ABG73779 standard; protein; 287 AA. ABG73779

03-APR-2003 (first entry)

Human NVR protein.

NVR; human; endothelial growth factor; cytostatic; cancer; angiogenesis; cell proliferation; revascularisation; amputation; vasculogenesis; transplant; brain; breast; intestine; kidney; lung; ovary; pancreas; prostate; uterus; gene therapy.

Homo sapiens

Location/Qualifiers

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New endothelial growth factor polypeptide and polynucleotides, useful for diagnosing, preventing, and treating cancer and other conditions or diseases involving angiogenesis and cell proliferation.
                 /note= "Encoded by TAA, an in frame stop codon which interrupts the coding region as shown in Figure 1A-B. This site is the end of the protein sequence represented in SEQ ID 1 of the Sequence listing" 282. 287 /note= "Region not represented in SEQ ID 1 of the Sequence Listing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel human endothelial growth factor polypeptide which has cytostatic activity. The polypeptide and its encoding polymucleotide are useful in the diagnosis, prevention, and treatment of cancer and other conditions or diseases involving angiogenesis and cell proliferation. NVR may also be used to promote revascularisation following traumatic amputation and surgical reconstruction or added to a tissue culture to promote vasculogenesis in tissues for autologous or heterologous transplant. Antagonists or this inhibitors of NVR may be used to suppress or prevent angiogenesis and brain, breast, intestine, kidney, lung, ovary, pancreas, prostate or uterus. The products of the invention can be used for gene therapy. This sequence represents the human NVR protein described in the disclosure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vascular endothelial growth factor; VEGF-D; angiogenesis; modification; acceleration; wound healing; tissue; organ; transplants; collateral circulation; infarction; arterial stenosis; coronary artery disease; inhibition; cancer; treatment; diabetic retinopathy; lung disorders; blood circulation; gaseous exchange; chronic obstructive airway disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                intestinal malabsorptive syndrome; biopsy; metastatic risk; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens vascular endothelial growth factor D (VEGF-D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW53240 standard; protein; 325 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 1A-B; 28pp; English.
                                                                                                                                                                                                                                                                                                                             Murry LE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                       09-JAN-2002; 2002US-00044622.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                      (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                         Goli SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 CNEESLIC 153
 Misc-difference 281
                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-182635/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CNEESLIC 8
                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ABQ77105
                                                                                                                                                    US2002155538-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 287 AA;
                                                                                                                                                                                                                                                     23-JAN-1997;
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                                                                                                                                                                                                                                                                                                                         Bandman O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW53240;
                                                                                    Region
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Human; angiogenic protein; wound healing; vascular tissue repair; peripheral arterial disease; critical limb ischaemia; coronary disease; angiogenesis; tumour; inflammation; diabetic retinopathy; psoriasis; theumatoid arthritis; autoimmune disease; allergy; cancer; therapy; infectious disease; neurodegeneration; vascular endothelial growth factor-D; VEGF-D.

Human VEGF-D protein sequence.

.158

(first entry)

05-APR-2001

AAY97572;

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/note= "potential N-linked glycosylation site"
156. 158
                                                 /note= "potential N-linked glycosylation site"
258. .260
                                                                 /note= "potential N-linked glycosylation site"
                                                                                                                                                                                                                                                                     Claim 16; Page 57-58; 101pp; English.
                                                                                                                                                                                    LUDWIG INST CANCER RES.
UNIV HELSINKI LICENSING LTD.
diagnosis; congestive heart failure.
                          Location/Qualifiers
                                                                                                                                                   97AU-00004954.
97US-0038814P.
                                                                                                                         96AU-00001825
                                                                                                                               96US-0023751P.
96AU-00003554.
                                                                                                                                            96US-0031097P
                                                                                                                                                                 97AU-00007435
                                                                                                                                                                       97US-0051426P
                                                                                                           97WO-US014696
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100..
                                                                                                                                                                                                        Achen MG, Wilks AF,
                                                                                                                                                                                                                      WPI; 1998-179057/16.
                                                                                                                                                                                                                              N-PSDB; AAV20806.
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 325 AA;
              Homo sapiens.
                                                                                 WO9807832-A1:
                                                                                                            21-AUG-1997;
                                                                                                                                                   05-FEB-1997;
10-FEB-1997;
                                                                                                                                                                        01-JUL-1997;
                                                                                                                         23-AUG-1996;
                                                                                                                                             14-NOV-1996;
                                                                                                                                                                 19-JUN-1997
                                                                                                                                     11-NOV-1996
                                                                                                                                                                                      (LUDW-)
                                                                                                                                                                                             (OYHE-)
                                                Region
                                   Region
                                                             Region
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Stacker SA, Alitalo K;

New nucleic acid encoding angiogenic proteins, useful e.g. for promoting healing of wounds and treating peripheral arterial disease, critical limb

ischemia or coronary disease

Ë Cao

Hu J,

Ruben SM,

Ковеп СА,

WPI; 2001-071057/08

N-PSDB; AAA91006

99US-0137796P.

03-JUN-1999;

(HUMA-) HUMAN GENOME SCI INC.

01-JUN-2000; 2000WO-US014925

WO200075163-A1

14-DEC-2000.

Homo sapiens.

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This sequence is vascular endothelial growth factor-D (VEGF-D), which is an angiogenic protein of the invention. The angiogenic proteins and the DNA sequences encoding them, are used to prevent, treat or ameliotate of disease and to detect diseases, or susceptibility, by detecting mutations or the presence or amount of angiogenic protein expression. Particularly cor the presence or amount of angiogenic protein expression. Particularly cor they are used to stimulate wound healing, growth of damaged bone and disease, critical limb ischaemia or coronary disease. Antagonists of the sequences are used to inhibit angiogenesis in tumours and to treat sequences are used to inhibit angiogenesis in tumours and to treat inflammation (where associated with increased vascular permeability), inflammation can expend (lymphangiogenesis. The proteins are also also useful for stimulating (lymphangiogenesis. The proteins are also and to raise antibodies. The antibodies are useful as therapeutic agents) cand to raise antibodies. The antibodies are useful as therapeutic or in vivo or in vitro diagnosis (including imaging) or for therapy correcting immunotyping of calls, e.g. for detection minimal residual disease or immunotyping of calls, e.g. for detection minimal residual disease or immunotyping of calls, e.g. for detection a very minimal residual disease or immunotyping be useful for treating a very wide range of other the antibodies and a very wide range of other the antibodies. The antibodies are useful for treating a very wide range of other the antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorders, e.g. autoimmune diseases; allergy; cancer; infectious diseases (viral, bacterial, fungal or parasitic); neurodegeneration, also as chemotactic agents or for stimulating regeneration of the nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 46; DB 4; Length 325; 100.0%; Pred. No. 4.6; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 226-227; 244pp; English.
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 325 AA;
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The sequence is that of human breast vascular endothelial growth factor D (VEGF-D). VEGF-D can be used for e.g. acceleration of angiogenesis in wound healing, tissue or organ transplantation, or to establish collateral circulation in tissue inferction or arterial stenosis, such as coronary artery disease, and inhibition of angiogenesis in the treatment of concer or of diabetic retinopathy. It can also be used in the creatment of lung disorders to improve blood circulation in the lungs and the blood stream or to improve blood circulation to the heart and 02 gas permeability in cases of cardiac insufficiency, to improve blood flow and gaseous exchange in che intestinal tract. Quantitation of VEGF-D in cancer blopsy in the intestinal tract. Quantitation of VEGF-D in cancer blopsy specimens may be useful as an indicator of future metastatic risk.

Antagonists can be used for treating e.g. conditions such as congestive heart failure, involving accumulations of fluid in the lung resulting from increases in vascular permeability. The products can also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated vascular endothelial growth factor-D - used to develop products for use in e.g. modifying angiogenesis or treating lung, heart or intestinal disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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0

Gaps

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117 CNEESLIC 124

qq ò

AAY97572 standard; protein; 325 AA.

RESULT 10 AAY97572 ID AAY9

117 CNEESLIC 124

8

1 CNEESLIC

8

8

1 CNEESLIC

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The present sequence represents a human zvegf2 growth factor encoded by the zvegf2 cDNA which was isolated from a human heart cDNA library.

Tvegf2 protein in a dimeric form acts as a mitogen for fibroblasts or smooth muscle cells. zvegf2 is claimed to be useful for stimulating the revascularisation of tissue or the re-endothelialisation of vascular clasue. zvegf2 is particularly claimed to be useful for the treatment of full-thickness skin wounds, including venous stasis ulcers and diabetic claimed achesives for promoting revascularisation of the healing tissue. Antagonists against zvegf2 can be used to block its mitogenic, chemotactic and angiogenic effects. The antagonists may therefore be useful for reducing growth of solid tumours by inhibiting neovascularisation of the developing tumour or by directly blocking tumour cell growth, in the treatment of diabetic retinopathy, psoriasis, arthritis, and scleroderma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vascular endothelial growth factor; VEGF-D; angiogenesis; modification;
                                                                                                                                                                                                                                                                                                                                                                                                     New isolated vascular endothelial growth factor - used to develop products for treating e.g. wounds, burns, myocardial infarction, tpsoriasis, arthritis, restenosis or organ transplants.
                                                                                                                                                                                                                                                                                                                                           Sheppard PO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 46; DB 2; Length 354; 100.0%; Pred. No. 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens vascular endothelial growth factor D (VEGF-D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                 /note= "Receptor binding domain"
                                                                                                                                                           /note= "Cysteine-rich domain""
                                                                                                                                                                                                                                                                                                                                        Nygaard S,
                                                                                                                                /note= "Balbiani ring motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                               "Cysteine-rich
                                                                                                       /note= "Balbiani ring
            24. .108
/note= "Pro-region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 53-54; 77pp; English.
                                                                                                                                                                                                                                                                                                                                        Hart CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW53241 standard; protein; 354 AA.
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97US-00933455
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                                                               .256
                                    .197
                                                                                         .274
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                                                                                                                                                                                                                                                                                                          (ZYMO ) ZYMOGENETICS INC.
                                                                            /note= '
257. .27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                       Conklin DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 CNEESLIC 153
                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-333256/29.
N-PSDB; AAV32823.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 354 AA;
                                   Binding-site
                                                                                                                                                                                      WO9824811-A2
                                                                                                                                                                                                                                         20-NOV-1997;
                                                                                                                                                                                                                                                                   06-DEC-1996;
18-SEP-1997;
                                                                                                                                                                                                                                                                                                                                   Gilbert T,
                                                                                                                                                                                                                11-JUN-1998
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           Peptide
                                                               Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents human vascular endothelial growth factor D (VEGF-D). The VEGF-D protein, compounds and antibodies, which can bind the protein, may be useful in, e.g. gene therapy and in treatment of inflammation and oedema. Vectors, containing the VEGF-D DNA, and VEGF-D DNA sequences may be used for screening for the compounds which bind to the VEGF-D protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human zvegf2 growth factor; mitogen; fibroblast; smooth muscle cell; venous stasis ulcer; diabetic ulcer; skin wound; chemotactic effect; angiogenic effect; tumour; diabetic retinopathy; psoriasis; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                     Human; vascular endothelial growth factor D; VEGF-D; gene therapy; inflammation; oedema.
                                                                                                                                                                                                                                                                                                                                                                                                        VEGF-D protein encoded by DNA - useful for, e.g. gene therapy and
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                                                                                                                                                                                                                                                                                                             (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
                                                                                                        Human vascular endothelial growth factor D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 46; DB
100.0%; Pred. No. 5;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .23
/note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 18-20; 52pp; Japanese.
                         AAW44293 standard; protein; 354 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW49036 standard; protein; 354 AA.
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                                                                                                                                                                                                                                                                                       96JP-00185216
                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                          Hirata Y, Nezu J;
                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAV15156.
                                                                                                                                                                                                                                                                                                                                                                                                                         treating oedema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 354 AA;
                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                      WO9802543-A1
                                                                                                                                                                                                                                                          15-JUL-1997;
                                                                                                                                                                                                                                                                                    15-JUL-1996;
                                                                             22-JUN-1998
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                                                    AAW44293;
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RESULT 11
         RESULT 12
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Gaps

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VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth; VEGD.

19-JAN-2001 (first entry)

Human VEGD protein.

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The sequence is that of human lung vascular endothelial growth factor D (VEGF-D). VEGF-D can be used for e.g. acceleration of angiogenesis in wound healing, tissue or organ transplantation, or to establish collateral circulation in tissue inferction or arterial stenosis, such as collateral circulation in tissue inferction or arterial stenosis, such as coronary artery disease, and inhibition of angiogenesis in the treatment of coronary artery disease, and inhibition of angiogenesis in the treatment of lung disorders to improve blood circulation in the lungs and/or gaseous exchange between the lungs and the blood stream or to improve blood circulation in the lungs and the blood stream or to cimcrove blood circulation to the heart and 02 gas permeability in cases of cardiac insufficiency, to improve blood flow and gaseous exchange in chronic obstructive airway disease, or to treat malabsorptive syndromes in the intestinal tract. Quantitation of VEGF-D in cancer bloops, specimens may be useful as an indicator of future metastatic risk. Antagonists can be used for treating e.g. conditions such as congestive heart failure, involving accumulations of fluid in the lung resulting from increases in vascular permeability. The products can also be used for treating e.g. conditions such as congestive from increases in vascular permeability. The products can also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vascular endothelial growth factor-D - used to developuse in e.g. modifying angiogenesis or treating lung, heart
acceleration, wound healing; tissue; organ; transplants; collateral circulation; infarction; arterial stemosis; coronary artery disease; inhibition; cancer; treatment; diabetic retinopathy; lung disorders; blood circulation; gaseous exchange; chronic obstructive airway disease; intestinal malabsorptive syndrome; biopsy; metastatic risk; detection; diagnosis; congestive heart failure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stacker SA, Alitalo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 16; Page 60-61; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNIV HELSINKI LICENSING LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated vascular endothelial
                                                                                                                                                                                                                                                                                                                                           96AU-00001825.
96US-0023751P.
96AU-00003554.
96US-0031097P.
97AU-00004954.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LUDW-) LUDWIG INST CANCER RES
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                                                                                                                                                                                                                                                                                                         97WO-US014696
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N-PSDB; AAV20807.
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                                                                                                                                                                                  Homo sapiens.
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05-FEB-1997;
10-FEB-1997;
19-JUN-1997;
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New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds.

Disclosure; Fig 11; 127pp; English.

Yon JR, Dijkmans JJH, Gosiewska A;

Sprengel JJ,

Xu J;

Dhanaraj SN,

Gordon RD,

WPI; 2000-442669/38

(JANC) JANSSEN PHARM NV

98GB-00028377. 99US-0124967P. 99US-0164131P.

99WO-US030503

21-DEC-1999; 22-DEC-1998; 18-MAR-1999; 08-NOV-1999;

29-JUN-2000

WO200037641-A2

Homo sapiens

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This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (IIa) and its encoding polynucleotide (IIa) which has unlinerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and antidabetic activity and actes as an angiogenesis and vascularization controlled antidabetic activity and actes as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ to preparing medicaments for treating wounds such as dermal ulcers, for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents the human VEGD protein used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 354;
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ive 0; Mismatches
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Mismatches

8; Conservative

Best_Local Similarity Matches 8; Conserv

Query Match

CNEESLIC 153

146

1 CNEESLIC 8

ð 셤 AAB10649 standard; protein; 354 AA.

RESULT 14 AAB10649

AAB10649

100.0%; Score 46; 100.0%; Pred. No. 5 ive 0; Mismatche

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Gaps

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Human; receptor tyrosine kinase; RTK; Flt4; fms-like tyrosine kinase 4; VEGFR-3; vascular endothelial growth factor receptor-3; chromosome 5q35; cytostatic; tumour imaging; anti-tumour therapy; treatment; diagnosis; neoplastic disease; lymphoma; carcinoma; breast; squamous cell; melanoma; sarcoma; malignancy; VEGF-D; vascular endothelial growth factor D.
                                                                                                                                                                                                                                                                                Treating neoplastic diseases such as lymphoma, carcinomas, melanomas and sarcomas, involves administering a compound capable of inhibiting binding of ligand proteins to fms-like tyrosine kinase-1 receptor.
Human prepro-vascular endothelial growth factor D.
                                                                                                                                                                                                                                         Valltola R, Jussila L;
                                                                                                                                                                                                                                                                                                                             Example 15-17; Page 142-143; 148pp; English.
                                                                                                                                                                                                  (LUDW-) LUDWIG INST CANCER RES. (UYHE-) UNIV HELSINKI LICENSING LTD OX.
                                                                                                                                                             99WO-US023525.
                                                                                                                                                                                 98US-00169079.
                                                                                                                                                                                                                                       Alitalo K, Kaipainen A,
                                                                                                                                                                                                                                                             WPI; 2000-317850/27.
                                                                                                             WO200021560-A1
                                                                                         Homo sapiens
                                                                                                                                                                                 09-OCT-1998;
                                                                                                                                                          08-OCT-1999;
                                                                                                                                     20-APR-2000.
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The patent discloses a method to treat neoplastic disease characterised by expression of fms-like tyrosine kinase 4 (Flt4) receptor (also referred as vascular endothelial growth factor receptor-3, VEGFR-3) in method involves administering a compound that inhibits binding of a ligand to Flt4 thereby inhibiting Flt4 mediated proliferation of vascular condothelial cells. The compound is useful for treating neoplastic disease such as breast carcinomas, squamous cell carcinomas, lymphomas, melanomas condothelial cells. The compound is useful for treating neoplastic disease and sarcomas. Flt4 receptor tyrosine kinase binding compounds can be used for manufacturing medicament useful for diagnostic screening, imaging and streatment of malignancies characterised by Flt4 expressing blood cells. The Flt4 gene maps to chromosomal region 535 and is expressed as 5.8 kb cand 4.5 kb mRNAs which differ in their 3 sequences and are confident of class III receptor tyrosine kinases (RTKS). It is used as a confident for tumour imaging and anti-tumour therapy. The present sequence is a human prepro-vascular endothelial growth factor D (VEGF-D), a compound a recombinantly matured VEGF-D and VEGFR-3 receptors and associate as non-covalently linked dimers

Sequence 354 AA;

0; 100.0%; Score 46; DB 3; Length 354; 100.0%; Pred. No. 5; Live 0; Mismatches 0; Indels Conservative Local Similarity Les 8; Conserv Query Match Matches

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Gaps

Search completed: September 5, 2004, 09:55:10 Job time: 27.2626 secs

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| cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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                                           ## Sequence 6, Application US/09761636A

## Patent No. US20020065218A1

## Sequence 6, Application US/09761636A

## Sequence 6, Application US/09761636A

## Sequence 6, Application US/09761636A

## APPLICANT: ATGHEN, Marc

## APPLICANT: HUGHEN, Richard

## APPLICANT: CENDRON, Angela

## APPLICANT: CENDRON, Angela

## APPLICANT: US/09/761,636A

## TITLE OF INVENTION: VGEFP-D/VEGF-D/VEGF

## CURRENT APPLICATION NUMBER: US/09/761,636A

## PRIOR APPLICATION NUMBER: US 60/176,293

## PRIOR APPLICATION NUMBER: US 60/176,293

## PRIOR PILING DATE: 2000-01-18

## PRIOR FILING DATE: 2000-01-16

## NUMBER OF SEQ ID NOS: 34

## SOFTWARE: PatentIn version 3.0

## SEQ ID NO 6

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; ORGANISM: Homo sapiens
US-09-761-636A-6
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Best Local Similarity
Matches 8; Conserv
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US-09-761-636A-6
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; Sequence 9, Application US/09761636A ; Patent No. US20020065218A1 CNEESLIC RESULT 2 US-09-761-636A-9 g

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patent No. US202010226041

patent No. US202010226041

patent No. US202010226041

general INFORMATION:

APPLICANT: ACHEN, Marc G.

APPLICANT: ACHEN, Marc G.

APPLICANT: ACHEN, Marc G.

APPLICANT: ACHEN, Marc G.

TITLE OF INVENTION: WASCULAR ENDOTHELIAL GROWTH FACTOR D EXPRESSION, FOR SCREENING TITLE OF INVENTION: VASCULARIZATION OF TISSUE

TITLE OF INVENTION: VASCULARIZATION OF TISSUE

TITLE OF INVENTION: VASCULARIZATION OF TISSUE

FILE REPERBNCE: 1064/48666PC

CURRENT FILING DATE: 2001-09-20

PRIOR APPLICATION NUMBER: 09/796, 714

PRIOR PILING DATE: 2001-09-20

PRIOR PILING DATE: 2000-09-20

PRIOR PILING DATE: 2000-09-20

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn version 3.1

SEQ ID NO 3

LENGTH. 10-0
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                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature; OTHER INFORMATION: Amino acid residues of Vall01-Pro196 of VEGF-D US-09-761-636A-1
                APPLICANT: HUGHES, Richard
APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VOGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT FILIG DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR PELICATION NUMBER: US 60/204,590
PRIOR FILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: US 60/204,590
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN VERSION 3.0
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Matches 8; Conservative
STACKER, Steven
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Best Local Similarity 100.
Matches 8; Conservative
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LENGTH: 96
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; Sequence 3, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
APPLICANT: ACHEN, Marc
APPLICANT: CENDROM; Angela
TILLE REPERENCE: 1064/48505 Achen et al
TILLE REPERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT PILING DATE: 2000-01-18
; PRIOR FILING DATE: 2000-01-18
; PRIOR FILING DATE: 2000-01-18
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PATENTIN UNBER: 33
; SOFTWARE: PATENTIN UNBER: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PATENTIN VERSION 3.0
; SEQ ID NO 3
       GENERAL INFORMATION:
APPLICANT: ACHEN, Marc
APPLICANT: STACKER, Steven
APPLICANT: CRACKER, Steven
APPLICANT: CRADRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 106505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN VEYERON 3.0
SOFTWARE: PATENTIN VEYERON 3.0
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; OTHER INFORMATION: Amino acid residues Vall01-Thr173 of VEGF-D
US-09-761-636A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 46; DB 9; Length 73; 100.0%; Pred. No. 0.66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 46; DB 9; Length 9; 100.0%; Pred. No. 1.2e+06;
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Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100...
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                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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US-09-761-636A-1
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APPLICANT: ACHEN, Marc

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TELEPHONE: 415-855-0555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIBRARY: LUNGASTO1
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: CA
COUNTRY: USA
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                                                                                                                                                                                                                                                                TYPE: PRT
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US-10-044-622-1
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Publication No. US20030211101A1
GENDEAL INFORMATION:
APPLICANT: Wise, Lyn M
APPLICANT: Savory, Lorden J
APPLICANT: Fleming, Stephen B
APPLICANT: Stacker, Stephen
TITLE OF INVENTION: VASCULAR ENOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF
     ENDOTHELIAL GROWTH FACTOR D, AND METHOD OF TREATING MELANOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/1079931
Sequence 1, Application US/1079931
GENERAL INFORMATION:
APPLICANT: ACHEN, Marc G.
APPLICANT: ACHEN, Marc G.
TILL OF INVENTION: ANTHEODIES TO TRUNCATED VEGF-D AND USES THEREOF CURRENT PLINGS DATE: 2004-02-18
FILE REFERENCE: ACHEN et al-1064-44660
CURRENT APPLICATION NUMBER: US/10/779,731
PRIOR APPLICATION NUMBER: US/10/100,037
PRIOR FILING DATE: 2002-03-19
PRIOR FILING DATE: 1999-12-21
PRIOR PLING DATE: 1999-12-21
PRIOR PLING DATE: 1999-12-21
PRIOR PLING DATE: 1999-12-21
PRIOR FILING DATE: 1999-05-17
PRIOR FILING DATE: 1999-05-17
SEQ ID NO: 1
ENGRETH Ver: 2.0
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                             CURRENT APPLICATION NUMBER: US/09/219,345A
CURRENT APPLICATION NUMBER: US/09/219,345A
CURRENT FILING DATE: 1998-12-23
FRIOR APPLICATION NUMBER: AU PP 1131
FRIOR APPLICATION NUMBER: US 60/087,392
FRIOR FILING DATE: 1998-12-24
FRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                              54 CNEESLIC 61
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Best Local Similarity
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TITLE OF INVENTION:
                                                                                                                                                                                               SEQ ID NO 1
LENGTH: 109
                                                                                                                                                                                                                                                                        US-09-219-345A-1
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US-10-779-731-1
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Gaps
TITLE OF INVENTION: VIRUS NZ2 BINDS AND ACTIVATES MAMMALIAN VEGF
TITLE OF INVENTION: RECEPTOR-2, AND USES THEREOF
FILE REPERBENCE: Sequence Listing for 09/431,833
CURRENT APPLICATION NUMBER: US/10/352,153
CURRENT FILING DATE: 2003-01-28
PRIOR PILING DATE: 1999-11-02
PRIOR FILING DATE: 1999-11-02
PRIOR PILING DATE: EARLIER FILING DATE: 1999-11-02
PRIOR PILING DATE: EARLIER FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIER FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 11
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
CORRUTAR: RESERVENTE DOS
SOFTWARE: FASTERN: DOS
CURRENT APPLICATION DATA:
FILING DATE: 09-Jan-2002
CIASSIFICATION PARA:
FRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/10044622
Publication No. US20020155538A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
Goli, Surya K.
Murry, Lynn E.
TITLE OF INVENTION: NOVEL ENDOTHELIAL GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/788,812
FILING DATE: «UNKNOWN-
ATORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REPERSTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0185 US
TELECOMMUNICATION INFORMATION:
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Sequence 3, Application US/10161694
Publication No. US20030125537A1
GENERAL INFORMATION:
APPLICANT: Andrew F. WILKS
Steven A. STACKER
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                                                                       100.0%; Score 46; DB 13; Length 280; 100.0%; Pred. No. 2.6; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEB: Evenson, McKeown, Edwards & Lenahan P.L.L.C. STREET: 1200 G Street, NW, Suite 700 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/Ms-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/10/274,953
FILING DATE: 22-cct-2002
CLASSIFICATION:
CLONE: 873352
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                    Sequence 3, Application US/10274953
publication No. US20030114658A1
GENERAL INFORMATION:
APPLICANT: Marce F. WILKS
APPLICANT: Steven A. STACKER
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/296,275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: DC COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 08/915,795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
REFREENCE/DOCKET NUMBER: 1064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
TISSUE TYPE: Human Breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: N/A INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (202) C-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                             Query Match
Best Local Similarity 100.
Matches 8; Conservative
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MOLECULE TYPE: protein
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US-10-044-622-1
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Sequence 2, Application US/09956095
Sequence 2, Application US/09956095
Patent No. US20020102260A1
GENERAL INFORMATION:
FAPLICANT: ACHEN, Marc G.
APPLICANT: STACKER, Steven A.
APPLICANT: STACKER, Steven A.
TITLE OF INVENTION: WESTHOODS FOR TREATING NEOPLASTIC DISEASE CHARACTERIZED BY
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR D EXPRESSION, FOR SCREENING
TITLE OF INVENTION: POR NEOPLASTIC DISEASE OR METASTATIC RISK AND FOR MAINTAINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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KART ALITALO
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSE: SUPERSON, MCKEOWN, Edwards & Lenahan P.L.L.C.
STREET: 1200 G Street, NW, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TSM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/09/296,275
FILING DATE: «UNKNOWN:
APPLICATION NUMBER: 08/915,795
FILING DATE: «UNKNOWN:
ATTORNEY/AGENT INFORMATION:
NAME: BVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/42983
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                               COUNTRY: United States of America ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/10/161,694
FILING DATE: 05-Jun-2002
CLASSIFICATION: <UNKNOWD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE TYPE: Human Breast
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 325 amino acids
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 8; Conservative
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RESULT 15
US-09-375-248-6
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APPLICANT: ACHEN, MARC
TITLE OF INVENTION: EXPRESSION VECTORS AND CELL LINES EXPRESSING VASCULAR
TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR D, AND METHOD OF TREATING
TITLE OF INVENTION: MELANOMAS
TITLE OF INVENTION: MELANOMAS
FILE REPERRING: 1064/44385 MARC ACHEN
CURRENT APPLICATION NUMBER: US/09/219,345A
CURRENT FILING DATE: 1998-12-23
PRIOR FILING DATE: 1998-12-24
PRIOR APPLICATION NUMBER: US 60/087,392
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PALCHLIN VOR: 2.0
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US-09-795-006A-119
i Sequence 119, Application US/09795006A
j Patent No. US_0020151680A1
j GENERAL INFORMATION:
i APPLICANT: Alitalo et al
i TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
i TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAS AND PROTEINS
i TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAS AND PROTEINS
i CURRENT FILING DATE: 2001-02-26
i PRIOR APPLICATION NUMBER: US 60/205,331
PRIOR FILING DATE: 2000-05-18
i PRIOR FILING DATE: 2000-05-25
i PRIOR FILING DATE: 2000-02-25
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TITLE OF INVENTION: VASCULARIZATION OF TISSUE FILE REFERENCE: 1064/48666pC
CURRENT APPLICATION NUMBER: US/09/956,095
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: 09/796,714
PRIOR PILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-09-20
PRIOR FILING DATE: 2001-09-20
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2001-09-20
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 354
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; Patent No. US20020127222A1
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Best Local Similarity 100.
Matches 8, Conservative
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                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-956-095-2
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US-09-219-345A-11
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LENGTH: 354
TYPE: PRT
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Sequence 6, Application US/09375248

Publication No. US20030026759A1

Publication No. US20030026759A1

Publication No. US20030026759A1

APPLICANT: Prezell, Robert E.

APPLICANT: Finegold, David N.

FILLE OF INVENTION: THE FITH RECEPTOR TYROSINE KINASE (VEGFR-3)

CURRENT APPLICATION NUMBER: US/09/375,248

CURRENT APPLICATION NUMBER: PCT/US99/06133

BARLIER PILING DATE: 1999-08-16

BARLIER PILING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 6

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100.0%; Pred. No. 3.3;
tive 0; Mismatches 0; Indels
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NUMBER OF SEQ ID NOS: 175
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 119
LENGTH: 354
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Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 8; Conservative
                                                                                  TYPE: PRT
; ORGANISM: Homo sapiens
US-09-795-006A-119
                                                                                                                                                                                                                                                                                                                     146 CNEESLIC 153
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Sequence 1, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 5, Appli
Patent No. 519439
Patent No. 519439
Sequence 15, Appl
Sequence 11, Appl
Sequence 2, Appli
Patent No. 5194596
Patent No. 519439
Patent No. 519739
Patent No. 5319739
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Sequence 8, Appli
                                                                          5, 2004, 09:55:30 ; Search time 7.11111 Seconds (without alignments) 58.079 Million cell updates/sec
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Sequence 33, 1
Sequence 15, 1
Sequence 20, 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1,6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-41-1888-8
US-09-41-1888-8
US-08-915-795-3
US-08-915-795-5
5194596-9
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5332671-3
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US-08-15-795-8
US-08-586-039B-33
US-09-699-769-33
US-08-669-769-31
US-08-569-063C-20
US-08-586-039B-31
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US-09-699-769-35
US-08-460-309-13
US-08-125-077-13
US-08-152-019A-29
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                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
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46
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Perfect score:
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No.
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Sequence 4, Appli Sequence 16, Appli Sequence 16, Appli Sequence 14, Appli Sequence 14, Appli Sequence 9, Appli Sequence 43, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 11, Appli	AND USES THEREOF	Length 109; Indels 0; Gaps 0;	AND USES THEREOF
1 US-08-144-121-4 4 US-08-735-893-4 4 US-09-562-702A-16 4 US-09-561-818A-16 4 US-09-561-818A-14 4 US-09-561-818A-14 4 US-09-561-818A-14 3 US-08-742-243-43 3 US-08-742-243-43 3 US-08-742-243-43 3 US-08-742-243-43 4 US-09-561-709B-9 5 US-09-561-709B-9 5 US-09-561-709B-11 6 US-09-574-708A-11 6 US-09-574-708A-11 6 US-09-574-708A-11 6 US-09-574-708A-11 6 US-09-574-708A-11 7 US-09-574-708A-11 7 US-09-574-708A-11 7 US-09-574-708A-11 7 US-09-574-708A-11 7 US-09-574-708A-11 7 US-09-574-708A-11	MENTS ATED VEGF-D 86	Score 46; DB 4; Pred. No. 0.33; 0; Mismatches 0;	RESULT 2 US-09-469-185-1 Sequence 1, Application US/09469185 Sequence 1, Application US/09469185 Parent No. 633188 SPACE INFORMATION: APPLICANT: ACHEN, MAXC G. APPLICANT: STACKER, Steve A. FILLE OF INVENTION: ANTIBODIES TO TRUNCATED VEGF-D; FILE REPERROKE: ACHEN et al-1064-44660 CURRENT APPLICATION NUMBER: US/09/469,185 CURRENT FILING DATE: 1999-12-21 EARLIER FILING DATE: 1998-12-21 EARLIER FILING DATE: 1999-05-17 EARLIER FILING DATE: 1999-05-17 EARLIER FILING DATE: 1999-05-17 SOFTWARE: PALENTIN OFF: 10005: 1 SOFTWARE: PALENTIN OFF: 2.0
71.7 1196 71.7 1196 71.7 1765 71.7 1765 71.7 1786 71.7 1786 69.6 12 69.6 12 69.6 100 69.6 110 69.6 110 69.6 110 69.6 110	RESULT 1 US-09-469-186-1 US-09-469-186-1 Sequence 1, Application US/09469186 Patent No. 6133434 GENERAL INFORMATION: APPLICANT: STACKER, Steve A. TILE PAPLICANT: ACHEN, MATC G. FILE REFERENCE: ACHEN et al.1064-44660 CURRENT APPLICATION NUMBER: US/09/469,12 CURRENT APPLICATION NUMBER: US/09-469,12 EARLIER FILING DATE: 1999-12-21 EARLIER FILING DATE: 1999-12-21 EARLIER FILING DATE: 1999-05-17 SOFTWARE: PATCH ON NUMBER: 60/134,556 BALLIER PILLING DATE: 1999-05-17 SOFTWARE: PATCH ON S: 1 SOFTWARE: PATCH ON S: 1 SOFTWARE: PATCH ON SI TYPE: PRT TYPE: PRT CORGANISM: HOMO SapienS	Similarity 100.0%. S. Conservative CNEESLIC 8	lication US/09 185. 186. 187. 187. 187. 187. 187. 187. 187. 187
	ULT 1 09-469-186-1 equence 1, Appl: equence 1, Appl: extent No. 638434 APPLICANT: STACK TITLE OF INVENTITYLE OF INVENTITYLE OF INVENTITYLE OF INVENTITYLE OF INVENTITYLE OF INVENTITYLE PEPERENCE: CURRENT APPLICAN SARLIER FILING I LENGTH: 109 TYPE: PRT LENGTH: 109 TYPE: PRT TYPE: PRT	fatc]	9-185-1 .ce 1, Applicat .no. 6531185 .no. 6531185 .canT: ACHEN, h .canT: ATHEN, TACKER, .canT: STACKER, .canT: STACKER, .canT: ATHEN .canT: ATHEN .canTion .
2	RESULT 1 US-09-469-1 Sequence Patent No GENERAL I APPLICAN TITLE OF FILE REF CURRENT CURRENT CURRENT EARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE SOFTWARE TYPE: P TYPE: P TYPE: P TYPE: P	Query Dest Lo	RESULT 2 US-09-469-11 Sequence Fatent No GENERAL II APPLICANT TITLE OF FILE REFE CURRENT FORENT FORE

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OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 20005
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APPLICANT: Wise, Lyn M
APPLICANT: Mercer, Andrew A
APPLICANT: Mercer, Andrew A
APPLICANT: Savory, Loreen J
APPLICANT: Stacker, Stephen
TITLE OF INVENTION: VASCULAR ENOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF
TITLE OF INVENTION: VASCULAR ENOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF
TITLE OF INVENTION: RECEPTOR-2, AND USES THEREOF
TITLE OF INVENTION: RECEPTOR-2, AND USES THEREOF
TITLE OF INVENTION: URGER: Sequence Listing for 09/431,833
Patent No. 6541008
CURRENT FILING DATE: 1999-11-02
EARLIER APPLICATION NUMBER: 60/106,809
EARLIER APPLICATION NUMBER: 60/106,800
EARLIER FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 11
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; Sequence No. 6235713
; Patent No. 6235713
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Steven A. STACKER
; APPLICANT: Steven B. STACKER
; APPLICANT: Steven B. STACKER
; APPLICANT: Steven A. STACKER
; APPLICANT: Steven B. STACKER
; APPLICANT: Wan ADDRESS:
; CORRESPONDENCE ADDRESS:
; STREET: 1200 G Street, NW, Suite 700
; CITY: Wanhington
; CITY: Wanhington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 46; DB 4; Length 197; 100.0%; Pred. No. 0.59; arive 0; Mismatches 0; Indels
                                                                                                                 100.0%; Score 46; DB 4; Length 109; 100.0%; Pred. No. 0.33;
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                                                                                                                                                                                                                                                                                                                                       US-09-431-888-8; Sequence B, Application US/09431888A; Sequence B, Patent No. 6541008; GENERAL INFORMATION:
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ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity 100.
Matches 8; Conservative
                                                                                                 Query Match
Best Local Similarity 100.
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US-09-431-888-8
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-469-185-1
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Gaps
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APPLICANT: Andrew F. WILKS
APPLICANT: Steven A. STACKER
APPLICANT: Steven A. STACKER
APPLICANT: STEVEN TITLE
APPLICANT: STEVEN TITLE
APPLICANT: STEVEN TITLE
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES:
ADDRESSES: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
STREET: 1200 G Street, NW, Suite 700
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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CAPUTER: ELADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ELADABLE FORM:
COMPUTER: ELADABLE FORMS:
COPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/915,795
FILING DATE:
CLASSIFICATION: 536
ATTONENT/AGENT INFORMATION:
NAME: EVANS, JOSEPH 26,269
REGISTRATION NUMBER: 26,269
REGISTRATION NUMBER: 26,269
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1000 628-8800
TELEFAX: (202) 628-8844
SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,795 FILING DATE:
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Patent No. 6235713
GENERAL INFORMATION:
                                                                                           CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH 106,
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064,
TELECOMMUNICATION INFORMATION:
TELECHONE: (202) 628-8800
TELECHONE: (202) 628-8844
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                                                                                                                                                                                                                                                              TELEFAX: ......
TELEX: N/A
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: protein
TYPE: NOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
TISSUE TYPE: Human Breast
US-08-915-795-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
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amino acid

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70 CNDESLEC 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 6; Conserv
                                                 JS-09-125-642C-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-125-642C-15
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US-09-431-888-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: TISCHER, EDMUND G.; ABRAHAM, JUDITH A.; FIDDES, JOHN C.; MITCHELL, RICHARD L.
JOHN TILLE OF INVENTION: DNA SEQUENCES ENCODING ENEGFIZO AND HUNGER 121 AND METHODS FOR THE PRODUCTION OF BOYINE AND HUNGAN VAASCULAR ENDOTHELIAL CELL GROWTH FACTORS, BVEGFIZO AND HVEGFIZI WINGER OF SEQUENCES: 40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/559,041
FILING DATE: 27-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 450,883
FILING DATE: 14-DEC-1989
PRIOR DATE: 27-JUL-1989
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                                                                                                                                                                                                                                                                                                  ;Patent No. 5194596;
APPLICANT: TISCHER, EDMUND G.;ABRAHAM, JUDITH A.;FIDDES, JOHN;C.;MITCHELL, RICHARD L.
TITLE OF INVENTION: PRODUCTION OF VASCULAR ENDOTHELIAL CELL
                                                                                                                                    100.0%; Score 46; DB 3; Length 354; 100.0%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 6; Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 6; Length 120;
Pred. No. 20;
                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36; DB 6
Pred. No. 20;
1; Mismatches
                                                                                                                                                                  0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                           GROWTH FACTOR

NUMBER OF SEQUENCES: 32

CURRENT APPLICATION DATA:

FILING DATE: 14-DEC-1989

FRIOR PAPLICATION DATE: 387,545

FILING DATE: 27-JUL-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.3%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.3%;
                                                                    ORIGINAL SOURCE:
TISSUE TYPE: Human Lung
US-08-915-795-5
                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                       MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
              single
                                                                                                                                                                                                                        CNEESLIC 153
                                                                                                                 Query Match
Best Local Similarity
-hes 8; Conserva
TYPE:
STRANDEDNESS: SINGA
                                                                                                                                                                                               1 CNEESLIC 8
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Best Local Similarity
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Best Local Similarity
Matches 6; Conserv
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;Patent No. 5219739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO:9:
LENGTH: 120
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                                                                                                                                                                                                                                                                       RESULT 6
5194596-9
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APPLICANT: Wise, Lyn M
APPLICANT: Warcer, Andrew A
APPLICANT: Savory, Loreen J
APPLICANT: Savory, Loreen J
APPLICANT: Steacher, Stephen B
APPLICANT: Fleming, Stephen B
APPLICANT: Steacher, Stephen B
TITLE OF INVENTION: VASCULAR ENOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF
TITLE OF INVENTION: VIRUS NZ2 BINNS AND ACTIVATES MAMMALIAN VEGF
FILE REFERENCE: Sequence Listing for 09/431,833
Patent NO. 6541008
Sequence 15, Application US/09125642C
Patent No. 6365393
GENERAL INFORMATION:
APPLICANT: BAYER AG
ITTLE OF INVENTION: Parapoxviruses Which Contain Foreign DNA, and
Their Production and Their Use in Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/EP97/00729,
FILING DATE: 17-Feb-97
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 4; Length 132;
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
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                                                                                                                                                                                                                                                                                                                                           ZIP: 15205-9741
COMPUTER READMBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/431,888A CURRENT FILING DATE: 1999-11.02
BARLIER APPLICATION NUMBER: 60/106,689
BARLIER FILING DATE: 1998-11.02
BARLIER APPLICATION NUMBER: 60/106,800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN: D1701 VEGF- Protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                                                                                                          NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: Bayer Corporation
STREET: 100 Bayer Road
CITY: Pittsburgh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSB: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/09431888A Patent No. 6541008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Parapox ovis
                                                                                                                                                                                                                                                                                             STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.3%;
75.0%;
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60 CNDESLEC 67
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                                                                                                 60 CNDESLEC 67
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                                                                           1 CNEESLIC 8
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;Patent No. 5219739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Patent No. 5332671
                                                                                                                                                         5219739-17
;Patent_No. 5219739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGIH: 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 164
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             Query Match
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5332671-3
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APPLICANT: Wise, Lyn M
APPLICANT: Wercer, Andrew A
APPLICANT: Bavory, Loren J
APPLICANT: Bavory, Loren J
APPLICANT: Stacker, Stephen
APPLICANT: Stacker, Stephen
TITLE OF INVENTION: VACULAR ENOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF
TITLE OF INVENTION: RECEPTOR-2, AND USES THEREOF
TITLE OF INVENTION: RECEPTOR-2, AND USES THEREOF
TITLE OF INVENTION: RECEPTOR-2, AND USES THEREOF
TITLE OF INVENTION: NUMBER: US/09/431,888A
CURRENT FILING DATE: 1999-11-02
CURRENT FILING DATE: 1998-11-02
EARLIER FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 2
LENGIH: 133
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5194596-17

FRECHT NO. 5194596

1. APPLICATION

C., MITCHELL, RICHARD L.

GROWTH FACTOR

NUMBER OF PROLUCTION OF VASCULAR ENDOTHELIAL CELL

GROWTH FACTOR

MUNDER OF PALICATION DATA:

APPLICATION NUMBER: US/07/450,883

FILING DATE: 14-DEC-1989

PRICH APPLICATION DATA:

APPLICATION NUMBER: 387,545

FILING DATE: 27-JUL-1989
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                                                                                                                                             Score 36; DB 4; Length 132;
Pred. No. 22;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                               S-09-431-888-2
Sequence 2, Application US/09431888A
Patent No. 6541008
GENERAL INFORMATION:
EARLIER FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.3%;
75.0%;
                                                                                                                                                  78.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                  Query Match 78.3
Best Local Similarity 75.0
Matches 6; Conservative
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                                                                                                                                                                                                                   1 CNEESLIC 8
                                                                                   ; TYPE: PRT
; ORGANISM: Orf virus
US-09-431-888-11
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US-09-431-888-2
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                                                 Gaps
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JOHN C.;MITCHELL, RICHARD L.

JUGHN C.;MITCHELL, RICHARD L.

TITLE OF INVENTION: DNA SEQUENCES ENCODING BYEGF120 AND

JHVEGF 121 AND METHODS FOR THE PRODUCTION OF BOVINE AND HUMAN

JAASCULAR ENDOTHELIAL CELL GROWTH FACTORS, BYEGF120 AND HVEGF121

NUMBER OF SEQUENCES: 40

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 40

FILING DATE: 27-JUL-1990

PRIOR APPLICATION NUMBER: 450, 883

FILING DATE: 14-DEC-1989

APPLICATION NUMBER: 387,545

FILING DATE: 27-JUL-1989
                                                                                                                                                                                                                                                                                         **PELICANT: TISCHER, EDMUND G.; ABRAHAM, JUDITH A.; FIDDES,
JOHN C.; MITCHELL, RICHARD L.
JOHN C.; MITCHELL, RICHARD L.
JTLE OF INVENTION: DNA SEQUENCES ENCODING BUGGF120 AND
JHUGGF 121 AND METHODS FOR THE PRODUCTION OF BOYINE AND HUMAN
'VAASCULAR ENDOTHELIAL CELL GROWTH FACTORS, BUEGF120 AND HUGGF121
'NUMBER OF SEQUENCES: 40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/559,041
FILING DATE: 27-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 450,883
FILING DATE: 14-DEC-1989
SPILICATION NUMBER: 387,545
FILING DATE: 27-JUL-1989
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Pred. No. 27;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 6; Length 164;
Pred. No. 27;
78.3%; Score 36; DB 6; Length 164; 75.0%; Pred. No. 27; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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75.08;
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75.0%;
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Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                               Best Local Similarity 75.0
Matches 6; Conservative
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APPLICANT: FERRARA, NAPOLEONE; LEUNG, DAVID W.H.
GROWTH FACTOR AND DNA ENCODING SAME
NUMBER OF SEQUENCES: 15
CURRENT APPLICATION DATA:
FILLING DATE: 04-MQ-1989
PRIOR APPLICATION NUMBER: 369,424
FILLING DATE: 21-JUN-1989
FILLING DATE: 21-JUN-1989
FILLING DATE: 21-JUN-1989
FILLING DATE: 12-MAY-1989
FILLING DATE: 12-MAY-1989
FILLING DATE: 12-MAY-1989
                                                                                                                                                                                                                                                                                                                                             Score 36; DB 6; Length 190;
Pred. No. 32;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
STREET: 1200 G Street, NW, Suite 700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.3%; Score 36; DB 3; Length 321; 62.5%; Pred. No. 53;
                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTEY: United States of America
ZIP: 20005
COMPUTER: DOORS
COMPUTER: IBM PC COMPATION TYPE: Floppy disk
COMPUTER: IBM PC COMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/08915795;
Patent No. 6235713;
GENERAL INFORMATION:
APPLICANT: Marc G. ACHEN
APPLICANT: Steven A. STACKER
APPLICANT: Steven A. STACKER
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFRENCE/DOCKET NUMBER: 1064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEPHONE: (202) 628-8844
                                                                                                                                                                                                                                                                                                                                             78.3%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: N/A INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 321 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; TISSUE TYPE: Mouse Lung
US-08-915-795-9
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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CLASSIFICATION: 536
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86 CNDESLEC 93
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                             LENGTH: 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-08-915-795-9
                                                                                                                                                                                                                                                        SEQ ID NO:3:
                                                                                                                                                                                                                                                                                               5332671-3
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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search,
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protein
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5, 2004, 09:47:29; Search time 8.4444 Seconds (without alignments) 125.302 Million cell updates/sec September Run on:

US-09-761-636A-7 61 1 CISVPLTSVPC 11 score: Sequence: Title: Perfect

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ription	hynothetical prote	. –	. "				brane		prof	prot		щ	Cation-transportin	nrobable component	֓֞֜֜֜֜֝֓֜֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֡֓֓֡֓֓֓֓֓֓֓֡֓֡֓֡֓֡		hypothetical proce		٦,				4		metalloproteinase	handthetical prote	t	inguioxypeiiz vnothetical	prot
SUMMARIES	ID	0	A72466	706	2931	46	31992	62018	T29234	34239	96814	85135	70592	G64707	E71813	T20160	B72727	JV0046	16392	T46975	64367	G71496	E72785	A59047	A35685	46964	4	16	975	514
		1 124	ΚŢ		H	H	٢	ß										_					2 E				T3			12
	h DB																													
	Length	151	16	207	92	106	35	50.	61	182	18	52,	583	788	786	178.	16	174	26	533	23,	95	112	11	20.	20.	296	305	308	342
.	Match	63.9	63.9	63.9	•	'n.	•		62.3	N	ö.	ö	0		٥.	60.7	φ,	59.0	9	59.0	6	59.0	7.	7.	57.4	57.4	57.4	57.4	57.4	57.4
	Score	39	39	39	39	39	38	38	38	38	37	37	37	37	37	37	36	36	36	36	36	36	35	35	32	35	35	35	35	35
+1,1300	No.	-1	7	e	4	Ŋ	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

	hypothetical prote	Origin recognition	atreptomycia biony	hypothetical prote	nrobable glucosylt	hypothetical prote	hypothetical prote	hypothetical prote	Gem-interacting nr	hypothetical prote	Genome nolymptein	hypothetical prote	nrobable ARC trans	prohable linoprote	probable lipoprote	hypothetical 8.6K
i c	TAREL	T02522	C75405	T19995	B84725	T48599	T20109	T25095	D59435	T16283	JC5620	T00826	A84845	C90971	H90901	JE0003
c	V	~	N	N	7	N	7	0	~	0	Н	N	~1	7	~	7
Ċ	3 4 7 7	363	403	410	457	537	756	790	970	1099	3014	1246	1816	61	61	92
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ŗ	n	57.	57.	57.	57.4	57.	57.	57.	57.	57.	57.	56.	56.	55.	55.	55.
7.0	n	35	35	35	35	35	35	35	35	35	35	34.5	34.5	34	34	34
6	2	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

virus F12

A,Cross-references: GB:M88588; NID:g333522; PIDN:AAA47188.1; PID:g333525 A;Note: submitted to the EMBL Data Library, May 1992

Gaps . 0 Query Match 63.9%; Score 39; DB 2; Length 151; Best Local Similarity 50.0%; Pred. No. 11; Matches 5; Conservative 4; Mismatches 1; Indels 1 CISVPLTSVP 10 ð

0

||::|:| 90 CINIPIDSIP 99 a

hypothetical protein APE2372 - Aeropyrum pernix (strain XI)
C:Species: Aeropyrum pernix
C:Species: 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: A7246
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kawarabayasi, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kawarabayasi, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kawarabayasi, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kawarabayasi, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kawarabayasi, M.; Kasidus: A; Reference number: A7456
A; Reference number: A72466
A; Returns: preliminary
A; Residus: Preliminary
A; Residus: 1-169 < Kawa

Gaps ·; 63.9%; Score 39; DB 2; Length 169; 60.0%; Pred. No. 12; ive 2; Mismatches 2; Indels Query Match 63.9 Best Local Similarity 60.0 Matches 6; Conservative

.; 0

1 CISVPLISVP 10

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A;Experimental source: adult testis; clone DKF2p434N1427 C;Genetics:
A;Note: DKF2p434N1427.1
                                                                                                  63.9%;
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Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                    Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CISVPLTSVPC 11
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                                                                                                                                                                                             3 SVPLTSVPC 11
                                                                                                                                                                                                                       25 SIPLSSTPC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: CESP: C49D10.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position:
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                                                                                                                               Cipacies: Sus scrofa domestica (domestic pig)

Cipacies: Sus scrofa domestica (domestic pig)

Cipacies: Out scrofa (domestic pig)

Cipacies: Out scrota (domestic pig)

Andoh, N.; Takeya, T.; Sato, B.

Mol. Cell. Endocrinol. 83, 65-71, 1992

A, Andoh, N.; Takeya, T.; Sato, B.

A, Reference number: 147061; MUID:92201478; PMID:1312961

A, Reference number: 147061; MUID:92201478; PMID:1312961

A, Residual type: MRNA

A, Molecule type: MRNA

A, Residuales: 1-207 crans

C, Superfamily: metalloproteinase inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Gene: CESP:F36D4.3
A.Map position: 5
A.Introns: 24/3; 56/2; 103/3; 187/1; 387/2; 429/3; 455/3; 516/1; 555/1; 782/2; 882/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein DKPZp434N1427.1 - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: T4644
R;Bloecker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23032
A;Accession: T46444
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A;Molecule type: DNA
A;Residues: 1-925 < RBJL:
A;Cross-references: EMBL: 915181; PIDN:AAA93485.1; GSPDB:GN00023; CESP:F36D4.3
A;Experimental source: strain Bristol N2; clone F36D4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: T29311
R;Pauley, A.; Gattung, S.
submitted to the EMBL Data Library, March 1996
A;Description: The sequence of C. elegans cosmid F36D4
A;Reference number: Z20603
A;Accession: T29311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 63.9%; Score 39; DB 2;
Best Local Similarity 54.5%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39; DB 2;
Pred. No. 64;
5; Mismatches
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50.0%;
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A;Molecule type: mRNA
A;Residues: 1-1062 <AAA>
A;Cross-references: EMBL:AL137701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 63.9
Best Local Similarity 50.0
Matches 5; Conservative
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2 VSLPMSNVPC 11
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                   57 CIGIPVASVP
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probable membrane protein YDR539w - yeast (Saccharomyces cerevisiae)

N.Alternate names: hypothetical protein D3703.2

Cybrecies: Saccharomyces cerevisiae
Cybrecies: 3accharomyces cerevisiae
Cybrecies: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 19-Apr-2002
Cybrecies: 562018

R;Dietrich, F.S.; Mulligan, J.; Allen, E.; Araujo, R.; Aviles, E.; Berno, A.; Carpenter, H.; Lin, D.; Mosedale, D.; Nakahara, K.; Namath, A.; Oefner, P.; Oh, C.; Petel, F.X.; R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            usubmitted to the EMBL Data Library, December 1995
A;Reference number: 862017
A;Accession: 562018
A;Accession: 562018
A;Accession: 562018
A;Accession: 562018
A;Accession: DNA
A;Residues: 1-503 < DIE>
A;Cross-references: EMBL: U43834; NID:g1165292; PID:g1165294; GSPDB:GN00004; MIPS:YDR5394
A;Experimental source: strain AB972
C;Genetics: A;Cross-references: SGD:S0002947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:AF016665; PIDN:AAC71178.1; GSPDB:GN00020; CESP:C49D10.3
A;Experimental source: strain Bristol N2; clone C49D10
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                          C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Bate: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
C.Batcession: T31992
R.Henkhaus, J.; Wohldmann, P.; Beck, C.
R.Henkhaus, J.; Wohldmann, P.; Beck, C.
R.Henkhaus, T.; Wohldmann, P.; Beck, C.
R.Henkhaus, T.; Wohldmann, P.; Beck, C.
R.Henkhaus, T.; Wohldmann, P.; Beck, C.
R.Heference to the EMBL Data Library, July 1997
A.Reference number: Z21108
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Length 1062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.3%; Score 38; DB 2; Length 324; 54.5%; Pred. No. 34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Map position: 4R
C;Superfamily: conserved hypothetical protein sll0936
C;Keywords: transmembrane protein
F;210-226/Domain: transmembrane #status predicted <TMM>
                                                                     1;
                                                                                                                                                                                                                                                                                                                                                   hypothetical protein C49D10.3 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: T31992
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-324 <HEN>
Score 39; DB 2;
Pred. No. 74;
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                                                              2; Mismatches
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hypothetical protein AT4g12650 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Eeb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001 Sprin 185135 (Spacession: H85135 (Spacession: H8
       ansen, N.F.; Hughes, B.; Huizar, L.
Mature 408, 816-820, 2000
Mature 408, 816-820, 2000
Mature 408, 816-820, 2000
Mature 408, 816-820, 2000
Mature 51, Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, E.; Kim, C.
C.A.; Li, J.H.; Eli, Y.; Marziali,
Matzo, M.; Ronney, D.; Sakano, H.
Maturers: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
Matiller, Sequence and analysis of chromosome 1 of the plant Arabidopsis.
Mathematical Mature 408-811; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable lpgB protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: F70592
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Atitle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Accession: F70592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GB: 295121; GB: AL123456; NID: 93261742; PIDN: CAB08345.1; PID: e314477;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GB: AE005173; NID: 94836878; PIDN: AAD30581.1; GSPDB: GN00141
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A) Status: prefilminary: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-583 <COL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 83;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60.7%; Scor.
100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150 PLTAVPC 156
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-184 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-527 <STO>
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A;Gene: T30F21.11
A;Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
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B96814
Bypothetical protein T30F21.11 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: B96814
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, Churg, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
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C.Species: Caenorhabditis elegans
C.Species: Os-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C.Accession: T34239
R.Wilson, R.; Bentley, D.; Gattung, S.
R.Wilson, R.; Bentley, D.; Gattung, S.
R.Wilson, The sequence of C. elegans cosmid F26F12.
A.Accession: T34239
A.Accession: T3429 WIL.>
A.Gross-references: EMBL:U55373; PIDN:AAC25894.1; GSPDB:GN00023; CESP:F26F12.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: CESP:F55G1.13
A;Map position: 4
A:Introns: 98/1; 136/1; 230/1; 256/1; 363/1; 401/1; 443/1; 484/1; 528/2; 551/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Cross-references: EMBL:US8750; PIDN:AAB00653.1; GSPDB:GN00022; CESP:F55G1.13
A.Experimental source: strain Bristol N2; clone F55G1
                                                                                                                                                                                                                                                          hypothetical protein F55G1.13 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T29234
R;Murray, J:; Le, T.T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38; DB 2; Length 616;
Pred. No. 65;
1; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                      R;Murray, J.; Le, T.T.
submitted to the BMBL Data Library, May 1996
A;Description: The sequence of C. elegans cosmid F55G1.
A;Reference number: Z20591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Experimental source: strain Bristol N2; clone F26F12 C; Genetics: A;Gene: CESP:F26F12.7 A;Map position: 5 A;Introns: 110/3; 441/3; 801/2; 1244/3; 1693/2; 1784/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-616 <MUR>
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|TVPVSSAPC 124
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2 ISVPLTSVPC 11
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Best Local Similarity
Matches 6; Conserv
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Matches 7; Conserv
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Query Match

456 CISVLVISCPC 466

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A; Experimental source: strain H37Rv

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A;Cross-references: EMBL:Z67881; PIDN:CAA91798.1; GSPDB:GN00028; CESP:T14G8.1 A;Experimental source: clone C52G5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, November 1995
A;Reference number: Z19955
A;Accession: T24924
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1787 <WI2>
A;Cross-references: EMBL:Z67884; PIDN:CAA91810.1; GSPDB:GN00028; CESP:T14G8.1
                                                                           hypothetical protein T14G8.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Dacies: L5-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Peb-2000
C;Accession: T20160; T24924
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A;Introns: 112/3; 453/3; 597/3; 815/2; 1258/3; 1682/2; 1709/3; 1764/1
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Pred. No. 2.8e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                submitted to the EMBL Data Library, November 1995
A;Reference number: 219231
A;Accession: T20160
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1787 <WIL>
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Best Local Similarity 60.07
Matches 6; Conservative
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Job time : 9.44444 secs
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A, Map position: X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        CjAccession: G64707

R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B. Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Reference number: A64520; MUD:97394467; PMID:9252185

A;Reference number: A64520; MUD:9739467; PMID:9252185

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Molecule type: DNA
A,Residues: 1-788 <TOM>
A,Residues: 1-788 <TOM>
A,Residues: 1-788 <TOM>
A,Cross-references: GB.AE000648; GB.AE000511; NID:g2314670; PIDN:AAD08539.1; PID:g231467
C,Superfamily: Enterococcus copper-transporting ATPase copA; ATPase nucleotide-binding of F;218-547/Domain: ATPase transduction domain homology <ATT>
F;612-750/Domain: ATPase nucleotide-binding domain homology <ATN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable component of cation transport for cbb3-type oxidase - Helicobacter pylori (stra
C,Species: Helicobacter pylori
A,Variety: strain J99
C,Date: 12-Feb-1999 #Bequence_revision 12-Feb-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-788 <ARN>
A;Cross-references: GB:AE001561; GB:AE001439; NID:g4156000; PIDN:AAD06962.1; PID:g41560d
A;Experimental source: strain J99
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C;Superfamily: Enterococcus copper-transporting ATPase copA; ATPase nucleotide-binding
F;612-750/Domain: ATPase nucleotide-binding domain homology <ATN>
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C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 11-Jan-2000
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Pred. No. 1.2e+02;
1; Mismatches 3; Indels
                                                                              60.7%; Score 37; DB 2; Length 583; 70.0%; Pred. No. 92; 1.ve 0; Mismatches 3; Indels
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Pred. No. 1.2e+02;
1; Mismatches 3;
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ilarity 63.6%;
Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
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                                                                                                                                         Conservative
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Best Local Similarity
7; Conserva
                                                                                                             Best Local Similarity
Matches 7; Conserv
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                                                                                    Query Match
C,Genetica:
A,Gene: lpqB
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Gaps

OM protein - protein search, using sw model

September 5, 2004, 09:38:39 ; Search time 5 Seconds
(without alignments)
114.554 Million cell updates/sec Run on:

US-09-761-636A-7

1 CISVPLTSVPC 11 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	1	1 rattu	043915 homo sapien	P97946 mus musculu	Sus	fow.		Sacch	P58021 mus musculu		Ol6102 drosophila				-	-	7	0	σ	o		ovis	-			Q8wyq5 homo sapien	homo	mus	_	55773	~		P24584 escherichia	ι. T
SUMMARIES	ID				VEGD_MOUSE	TIM1_PIG	V110 FOWPV	AIM1 HUMAN	YD39 YEAST	T9S2_MOUSE	T9S2_HUMAN	CHD3 DROME	CHD3 CAEEL	BB12_SCHCO	C5L2_HUMAN	SYK METJA	SYK METMP	ADAS_TRYBB	STNB_MOUSE	STNB_HUMAN	COMA CONMA	TIM1_BOVIN		RPC6_CAEEL	ORC2_ARATH			- 1			SY23 HUMAN			KPM2 ECOLI	LDH_THEMA
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## ALIGNMENTS

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EMBL; Y12870; CAA73:
EMBL; AJ000185; CAA(
EMBL; BC027948; AAH7
HSSP; P15692; 1VPP.
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                                                                                                                                                                                                                                                                                               VEGD HUMAN STANDARD; PRT; 354 AA.

043915;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced growth factor) (FIGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98140120; PubMed=9479493;
Rocchigiani M., Lestingi M., Luddi A., Orlandini M., Franco B.,
Rossi E., Ballabio A., Zuffardi O., Oliviero S.;
"Human FiGF: cloning, gene structure, and mapping to chromosome Xp22.1
between the PIGA and the GRPR genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Achen M.G., Jelesch M., Kukk E., Maekinen T., Vitali A., Wilks A.F., Alitalo K., Stacker S.A.; Hardran E., Stacker S.A.; Hardran Endothelial growth factor D (VEGF-D) is a ligand for the tyrosine kinases VEGF receptor 2 (Flk1) and VEGF receptor 3 (Flk4)."; Proc. Natl. Acad. Sci. U.S.A. 95:548-553(1998).
                                                                                                                                                                                                             Gaps
                                                                                           BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

INTERCHAIN (BY SIMILARITY).

INTERCHAIN (BY SIMILARITY).

INTERCHAIN (BY SIMILARITY).

INTERCHAIN (BY CONTINE).

INTERMED (GLCNAC. ...) (POTENTIAL).

N-LINKED (GLCNAC. ...) (POTENTIAL).
            POTENTIAL.
VASCULAR ENDOTHELIAL GROWTH FACTOR D.
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97349118; PubMed=9205122;
Yamada Y., Nezu J.-I., Shimane M., Hirata Y.;
"Molecular cloning of a novel vascular endothelial growth factor,
                                4 X 16 AA REPEATS OF C-X(10)-C-X-C-X(1,3)-C.
                                                                                                                                                                                                             ·.
                                                                                                                                                                                          70.5%; Score 43; DB 1; Length 326;
                                                                                                                                                                                                            0; Indels
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MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                       1261AFA373596C00 CRC64;
                                                                                                                                                                                                    Pred. No. 1.4;
                                                         (APPROXIMATE)
                                                                                                                                                                                                100.0%; Preq. ...
                                                                                     4 (INCOMPLETE)
                             POTENTIAL.
  POTENTIAL
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                                                                                                                                                                         37112 MW;
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|SVPLTSVP 181
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150
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326 AA;
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Best Local Similarity
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TISSUE=Lung;
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CARBOHYD
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Klausmer R.D., Caberne B. Bueter K.H.; Schaefer C.P.; Baht N.K.;

R. Scheiten B. F. Caberne B. Bueter R. A., Rubhin G.M.; Hong L.,

B. Stepleton M.; Source M.; Boraldo M. R.; Casavart T.L.; Scheefer T.E.;

R. Stepleton M.; Joarse M.B.; Donaldo M.F.; Casavart T.L.; Scheefer T.E.;

R. Stepleton M.; Joarse M.B.; Donaldo M.F.; Casavart T.L.; Scheefer T.E.;

R. Stepleton M.; Joarse M.B.; Donaldo M.F.; Casavart T.L.; Scheefer T.E.;

R. Stepleton M.; Joarse M.B.; Donaldo M.F.; Casavart R.D.; Millay S.J.;

R. Bask S.A.; McGwan P.J.; McGernan K.J.; Malan K.J.; Scheefer T.E.;

R. Bask S.M.; McGwan P.J.; McGernan K.J.; Malan M.; Doditiques S.; Sanchez A.;

R. Pallarei S.; Warth M. Ketteman M.; Wandan M. J.; Scheefer D.; Dickson M.C.;

R. Backliger A.C.; Grimwood J., Schmitz J.; Myers M.,

R. Butterfield W. Medan J., Younges S.J.; Myers M.,

R. Butterfield W. S.M.; McZyaninki M.I.; Skalase U.; Bmails D. E.;

R. Binnerth A.; Schlein J.E.; Ordes S.J.; Myers M. J.;

R. Bornerth A.; Schlein J.E.; Ordes S.J.; M.; Merra M.A.;

R. Schmerth A.; Schlein J.E.; Ordes S.J.; Moriz R., Karpann T.,

R. Milla R. K. A. Malan M. J. Sungson R.J.; Moriz R., Karpann T.,

R. Milla R. K. Rebeal M.G.; Sungson R.J.; Moriz R., Karpann T.,

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R. Milla R. W. Rebeal M.G.; Sungson R.J.; Moriz R., Karpann T.,

R. Milla R. W. Rebeal M.G.; Sungson R.J.; Mo
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Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced growth factor) (FIGF).
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                    SMART; SM00141; FUGE; 1.

PROSITE; PS00249; PDGF_1; 1.

PROSITE; PS50278; PDGF_2; 1.

Angiogenesis; Mitogen; Growth factor; Glycoprotein; Signal; Repeat; Cleavage on pair of basic residues; Multigene family.

21

POTENTIAL.

**MANOP FORM).
                                                                                                                                                                                                                                                  BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CS7BL/6J; TISSUE=Fibroblast;
MEDLINE=97030254; PubMed=8876195;
Orlandini M., Marconcini L., Ferruzzi R., Oliviero S.;
Identification of a c-fos-induced gene that is related to the platelet-derived growth factor/vascular endothelial growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
InterPro; IPR00453; CXCXC_repeat.
InterPro; IPR004073; PD_growth_factor.
Pfam; PF03128; CXCXC; 3.
Pfam; PF0341; PGFF; 1.
ProDom; PD001629; PD_growth_factor; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97349118; PubMed=9205122;
Xamada Y., Nezu J.-I., Shimane M., Hirata Y.;
"Molecular cloning of a novel vascular endothelial growth factor,
                                                                                                                                                                                  4 X 16 AA REPEATS OF C-X(10) -C-X-C-
                                                                                                                                                           VASCULAR ENDOTHELIAL GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                       ..
                                                                                                                                                                                                                                                                                                                                                                             Score 43; DB 1; Length 354; Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                     2048D769D735173E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 93:11675-11680(1996)
                                                                                                                                                                                                          (APPROXIMATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P97946;
28-FEB-2003 (Rel. 41, Created)
29-FEB-2003 (Rel. 41, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Preq. .v..
                                                                                                                                                                                                                                                                                                                                                    40444 MW;
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DEVELOPMENTAL STAGE.
                                                                                                                                                                                                                                                                                                                                                    354 AA;
                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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MEDINE-21276411; PubMed-11279005;
MEDINE-21276411; PubMed-11279001;
MEDINE-21276411; PubMed-11279001;
MEDINE-2127641; MEDINE-2127641; MEDINE-21276; MEDINE-2127641; MEDINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                            Avantaggiato V., Orlandini M., Acampora D., Oliviero S., Simeone A.; 
"Embryonic expression pattern of the murine figf gene, a growth factor belonging to platelet-derived growth factor/vascular endothelial growth factor family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vertebral column.

INDUCTION: By the transcription factor c-fos.

FINIURATION: By the transcription factor c-fos.

FINIURATION: By the transcription factor c-fos.

FINIURATION: By the transcription for marrial of the formation with increased activity toward VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer linked by disulfide bonds before secretion. The fully processed linked by disulfide bonds before secretion. The fully processed VEGF-D is composed mostly of two VEGF homology domains (VHDs) bound by non-covalent interactions (By similarity).

SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS02249; PDGF 1; 1.
PROSITE; PS50278; PDGF 2; 1.
Anglogenesis; Mitogen; Growth factor; Glycoprotein; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VASCULAR ENDOTHELIAL GROWTH FACTOR D. POTENTIAL.
4 X 16 AA REPEATS OF C-X(10)-C-X-C-X(1,3)-C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cleavage on pair of basic residues; Multigene family.
SIGNAL 1 21 PROPEP 22 93 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:108037; Figf.
GO; GO:0005576; C:extracellular; IDA.
GO; GO:0005083; F:growth factor activity; IDA.
GO; GO:0005515; F:growth factor activity; IDA.
GO; GO:0005283; P:cell proliferation; IPI.
InterPro; IPR004153; CXCXC_repeat.
InterPro; IPR000472; PD_growth_factor.
Pfam; PF00341; PDGF; 1.
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SMART; SM00141; PDGF; 1.
  MEDLINE=98288130; PubMed=9622638;
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EMBL; D89628; BAA14002.1; -.
HSSP; P15692; IVPP.
                                                                                                                                    Wech. Dev. 73:221-224 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PMMA-2DPAGE; P97946; -.
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                                                                                                                                                                                          RECEPTOR SPECIFICITY.
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PIR; 147061; 147061.
HSSP; P01033; 1UEA.
                                                                                                                                                                                                   SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang J.F., Boykiw R.H., Reno C.R., Hart D.A., Olson M.E.;
"Cloning and sequencing of porcine TIMPs.";
"Cloning and sequencing of porcine TIMPs.";
submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Complexes with metalloproteinases (such as collagenases)
and irreversibly inactivates them.
-!- SHDEELLULAR LOCATION: Secreted.
-!- PTM: The activity of TIMP1 is dependent on the presence of disulfide bonds.
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 34-195 FROM N.A. Manay J.B., Setton L.A.; ABar A.B., Kraus V.B., Setton L.A.; Bar A.B., Kraus G.B., G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=9220148, PubMed=1312961;
Tanaka T., Andoh N., Takeya T., Sato E.;
"Differential screening of ovarian cDNA libraries detected the expression of the porcine collagenage inhibitor gene in functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metāzoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                     N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
6636B17FBF07037C CRC64;
                                                                                                                                                                                                                                                                                 .
                                                                                                                                                                                                                                      Score 43; DB 1; Length 358;
Pred. No. 1.5;
0; Mismatches 0; Indels
    3.
4.
BY SIMILARITY.
BY SIMILARITY.
INTERCIAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIM1 PIG STANDARD; PRT; 207 AA. P35624; Q9TT83; Q9TTB9; 01-JUN-1994 (Rel. 29, Created) 1-GOCT-2001 (Rel. 40, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Metalloproteinase inhibitor 1 precursor (TIMP-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Belongs to the TIMP family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol. Cell. Endocrinol. 83:65-71(1992).
                                                                                                                                                                                                                                                               Local Similarity 100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, S96211; AAB21865.1; -.
EMBL, AF201726; AAF24348.1; -.
EMBL, AF156029; AAF17354.1; -.
                                                                                                                                                                                                       40908 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 37-144 FROM N.A. TISSUE=Skin;
                                                                                                                                                                                                                                            70.5%;
                                                                                                                                                                                                                                                                                                                                                           173 isverrsve 181
                                                                                                                                                                                                                                                                                                                          2 ISVPLTSVP 10
                                                                                                                                                                                 292
358 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI TaxID=9823;
      282
306
116
147
151
151
150
160
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      REPEAT
REPEAT
DISULFID
DISULFID
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CARBOHYD
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                                                                                                                                                CARBOHYD
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                                                                                                                           DISULFID
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TIM1_PIG
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MEDLINE=91139784; PubMed=8380837;
Ogawa R., Calvert J.G., Yanagida N., Nazerian K.;
"Insertional inactivation of a fowlpox virus homologue of the vaccinia virus F12L gene inhibits the release of enveloped virions.";
J. Gen. Virol. 74:55-64(193).
-: SIMILARITY: BELONGS TO THE POXVIRUSES F11 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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MEDLINE-20193820; PubMed=10729156;
MEDLINE-20193820; PubMed=10729156;
MEDLINE-20193820; PubMed=10.Z9156;
MITHE Genome of fowlpox virus.";
J. Virol. 74:3815-3831(2000).
                                                                                                                                                                                                                                       BY SIMILARITY.

METALLOPROTEINASE INHIBITOR 1.

BY SIMILARITY.

BY SIMILARITY.
                                                                                                                                                                          Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B04895846EB56BD0 CRC64;
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01-JUN-1994 (Rel. 29, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 4.7;
1; Mismatches
Interpro; IPR001820; TIMP.
Interpro; IPR008993; TIMP_like.
Pfam; PF00965; TIMP; 1.
PRART; SM0206; NTR; 1.
PROSITE; PS50199; NTR; 1.
PROSITE; PS00288; TIMP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23098 MW;
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                                                                                                                                                                                                                                                    23
207
147
1122
1122
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1189
101
101
101
101
86
                                                                                                                                                                                                                                                    Fowlpox virus (FPV)
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NCBI_TaxID=10261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein FPV110.
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CONFLICT
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BETA/GAMMA CRYSTALLIN 'GREEK

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Q03034;
                                                                                                                                                                              DOMAIN
SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
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             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the EMPL outstation and Emropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mabulars 123013; *Musuelsous):2, Meditzer P.S., Trent J.M.;
Ray M.E., Wistow G., Su Y.A., Meltzer P.S., Trent J.M.;
"AIM1, a novel non-lens member of the betagamma-crystallin
superfamily, is associated with the control of tumorigenicity in human
malignant melanoma.";
Proc. Natl. Acad. Sci. U.S.A. 94:3229-3234(1997)
-! FUNCTION: May function as suppressor of malignant melanoma. It may
exert its effects through interactions with the cytoskeleton.
-! SIMILARITY: Belongs to the beta/gamma-crystallin family.
-! SIMILARITY: Contains 12 beta/gamma crystallin 'Greek key' domains.
-! SIMILARITY: Contains 1 ricin B-type lectin domain.
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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KEY'
                                                                                                                                                                   63.9%; Score 39; DB 1; Length 451; 50.0%; Pred. No. 11; ive 4; Mismatches 1; Indels
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BETA/GAMMA CRYSTALLIN 'GREEK
BETA/GAMMA CRYSTALLIN 'GREEK
BETA/GAMMA CRYSTALLIN 'GREEK
                                                        PIR; PQ0506; PQ0506.
InterPro; IPR007027; Pox F11.
Pfam; PF04943; Pox F11; I.
SEQUENCE 451 AA; 52010 MW; 664623EA83D3A331 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001064; Crystallin.
InterPro; IPR000772; Ricin B lectin.
InterPro; IPR000772; Ricin B lectin.
Pfam; PF00030; crystall; B.
Pfam; PF00052; Ricin B lectin; 3.
PRINTS; PR01367; BGCRYSTALLIN.
SMART; SM00458; RICIN; 1.
SMART; SM0047; XTALD9; 6.
PROSITE; PS50915; CRYSTALLIN BETAGAMMA; 12.
PROSITE; PS50915; RICIN B LECTIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Liver;
MEDLINE=97250519; PubMed=9096375;
                   EMBL; AF198100; AAF44454.1; -. EMBL; M88588; AAA47188.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                AIM1 HUMAN STANDARD; E Q9Y4K1; 000296; 16-0CT-2001 (Rel. 40, Last sequin-0-CT-2003 (Rel. 42, Last anno-cot-2003 (Rel. 42, Last anno-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Absent in melanoma 1 protein.
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EMBL; U83115; AAB53791.1; -.
                                                                                                                                                                                                               5; Conservative
                                                                                                                                                                                                                                                    1 CISVPLTSVP 10
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90 CINIPIDSIP 99
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Genew; HGNC:356; AIM1.
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1163
1206
                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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1123
1164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E., Berno A., Carpenter J., Chen B., Cherry J.M., Chung E., Duncan M., Hunicke-Smith S., Hyman R., Komp C., Kashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., Petel F.X., Roberts D., Schramm S., Schroder M., Shogren T., Shroff N., Winant A., Yelton M., Botstein D., Davis R.W.; Submitted (DEC-1995) to the BMBL/GenBank/DbBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
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30-MAY-2000 (Rel. 39, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical 56.2 kDa protein in PADI-YRF1 intergenic region.
BETA/GAMMA CRYSTALLIN 'GREEK KE
                                                                                                                                                                                                                                                      63.9%; Score 39; DB 1; Length 1723;
45.5%; Pred. No. 45;
Live 3; Mismatches 3; Indels
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                                                                                                                                                                                                         7E50F681A627FB09 CRC64;
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503 AA; 56164 MW; 379B19319930BB4F CRC64;
                                                                                                                                                                                 RICIN B-TYPE LECTIN
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Germonline; 141031; .

SGD; S0002947; YDR339W.

InterPro; IPR002830; carboxylyase.

Pfam; PF01977; Ublb; 1.

TIGRFAMS; TIGR00148; TIGR00148; 1.

Hypothetical protein.
             EMBL; U43834; AAB64981.1; -.
                                                                                                                                                                                                                                                                                                           Conservative
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481 CVQSPISSFPC 491
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115 ITVPVSSAPC
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Best Local Similarity
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Best Local Similarity
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                                                                               Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                         TRANSMEMBRANE 9 SUPERFAMILY PROTEIN
                                                                                                                                                                                                                                                  (Probable).
-!- SIMILARITY: Belongs to the nonaspanin (TM9SF) family.
           16-0cT-2001 (Rel. 40, Created)
16-0cT-2001 (Rel. 40, Last sequence update)
10-0cT-2003 (Rel. 42, Last annotation update)
Transmembrane 9 superfamily protein member 2 precursor.
                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL)
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662 AA.
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PRT;
                                                                                                                                                                                                                                                                                                                    EMBL; BC003862; AAH03862.1; -.
                                                                                                                                                                                                                                                                                                                         MGD; MGI:1915309; Tm98f2.
InterPro; IPRO04240; EMP70.
Pfam; PF02990; EMP70; 1.
Signal; Transmembrane.
SIGNAL
STANDARD;
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465
486
521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Probable).
-!- TISSUB SPBCIFICITY: Ubiquitously expressed. Especially abundant in panoreas, highly expressed in kidney, lower levels in heart, brain, skeletal muscle and placenta. Lowest expression in lung and
                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=9838453; PubMed=9729438; MEDLINE=98398453; PubMed=9729438; Schimmoeller F., Diaz B., Muehlbauer B., Pfeffer S.R.; Schimmoeller F., Diaz B., Muehlbauer B., Pfeffer S.R.; Characterization of a 76 kDa endosomal, multispanning membrane protein that is highly conserved throughout evolution."; Gene 216:311-318(1998).

-:- FUNCTION: In the intracellular compartments, may function as a channel or small molecule transporter.

-:- SUBCELLULAR LOCATION: Integral membrane protein. Endosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEMBRANE 9 SUPERFAMILY PROTEIN
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16-0cT-2001 (Rel. 40, Last sequence update)
16-0cT-2001 (Rel. 40, Last annotation update)
Transmembrane 9 superfamily protein member 2 precursor (p76).
                                                                                                      Score 38; DB 1; Length 662;
Pred. No. 25;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Belongs to the nonaspanin (TM9SF) family.
                                  CYTOPLASMIC (POTENTIAL).
85F113A5D21733E7 CRC64;
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GO; GO:0005768; C:endosome; TAS.

GO; GO:0005887; C:integral to plasma membrane; TAS.

GO; GO:0006810; P:transport; TAS.

Interpro; IPR004240; EMP70.

Fignal; Transmebrane.

Signal; Transmebrane.
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LUMENAL (POTENTIAL).
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                                                                   75329 MW;
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                                                                                                             62.3%;
77.8%;
                                                                                                                                                           7; Conservative
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                                                                   662 AA;
                                                                                                                                    Local Similarity
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                                                DOMAIN
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                                                                                                                                                             Matches
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R. SENDINGE KNOWN N.A.

R. SENDINGE-2019 6006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holf P.W., Hoskins R.A., Galle R.F.,

RA Adams M.D., Celniker S.E., Holf P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Berndon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C.R., Baldwin D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Barendale J., Bayraktaroglu L., Beasley E.M.,

RA Besson K.Y., Benos P.V., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Grery J.M., Cawley S., Dallke C., Davenport L.B., Dolshakov S.,

RA Grery J.M., Cawley S., Dallke C., Davenport L.B., Durics P.M.,

RA Grery J.M., Cawley S., Dallke C., Davenport L.B., Durics P.,

RA Grery J.M., Cawley S., Dallke C., Davenport L.B., Durics P.,

RA Grery J.M., Cawley S., Dallke C., Davenport L.B., Durics P.,

RA Grery J.M., Cawley S., Dallke C., Perraca C., Ferriera S., Plunkov B.C., Dunn P.,

RA Grery J.M., Cawley S., Dallke C., Perraca C., Ferriera S., Plaischman W.,

RA Godson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,

Hostin D., Houston K.A., Howland T.J., Well M., Ill Z., Lidang Y., Lin X.,

RA Harris N.L., Harvey D.A., Heiman T.J., Welly M.-H., Ibeyar R.

RA Harkulov G., Milshina N.V., Nobary C., Morris J., Mosher D.L.,

RA Alali M., Malson M.V., Nixon K., Nurskern D.R., Pacher M. G.,

RA Alazzolo M., Pitten K.A., Nixon K., Nurskern D.R., Pacher M. Shuc B.

RA Rainert K., Remington K., Saunders R., Weissenbach J.M., Wang X.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Nurby R.,

RA Wang Z.-Y., Wassarama D.A., Weinstock G.M., Weissenbach H.,

RA Walliams S.M., Woodage T., Worley K.C., Mu D., Yang S., Yao Q.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                              Score 38; DB 1; Length 663; Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                         POTENTIAL.
CYTOPLASMIC (POTENTIAL).
C21A4D224534734D CRC64;
                                    CYTOPLASMIC (POTENTIAL)
                                                                                                                                                   CYTOPLASMIC (POTENTIAL)
                                                 POTENTIAL.
                                                                                                                                                                                                          LUMENAL (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          892 AA
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18s 7; Conservative
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CISVPLTFI 487
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        Zhu X., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Berkeley; TISSUB=Embryo;
MEDLINE=22426066; PubMed=12537569;
Stapheron M., Carlson J.W., Brokstein P., Yu C., Champe M.,
Garin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
Rubin G.M., Celniker S.E.;
"A Drosophila full-length cDNA resource.";
Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
                                                                                                                                      Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whittield E.J., Bayraktaroglu L., Berman B.P. Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Characterization of the CHD family of proteins.";
"Characterization of the CHD family of proteins.";
Proc. Natl. Acad. Sci. U.S.A. 94:11472-11477(1997).
-!- FUNCTION: Possible transcription activator (By similarity).
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: Belongs to the SNF2/RAD54 helicase family.
-!- SIMILARITY: Contains 2 chromo domains.
-!- SIMILARITY: Contains 1 PHD-type zinc finger.
-!- CAUTION: Ref.3 sequence differs from that shown due to a stop codon in position 628 and a frameshift in position 720.
-- CAUTION: Ref.4 sequence differs from that shown due to cloning
                                                                                                                                                                                                                                                                                 "Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0005634; C:nucleus; ISS.
GO; GO:0003682; F:chromatin binding; ISS.
GO; GO:0004386; F:helicase activity; ISS.
GO; GO:0006333; P:chromatin assembly/disassembly; NAS.
                                                                                                                                                                                                                                                                                                        systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
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InterPro; IPR001650; Helicase_C.
InterPro; IPR00130; SNRZ N.
InterPro; IPR00130; SNRZ N.
InterPro; IPR001965; Znf PHD.
Pfam; PF00621; helicase_C; 1.
Pfam; PF00628; PHD; 1.
SMART; SM00298; CHROMO; 2.
SMART; SM00480; HELICC; 1.
SMART; SM00480; HELICC; 1.
SMART; SM00490; HELICC; 1.
SMART; SM00249; PHD; 1.
PROSITE; PS000599; CHROMO 1; FALSE_NEG.
PROSITE; PS00013; CHROMO_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE003517; AAF49162.2; -.. EMBL; AY071503; AAL49125.1; ALT FRAME. EMBL; AF007780; AAB87384.1; ALT_SEQ.
                                                                                                                     MEDLINE=22426069; PubMed=12537572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-812 FROM N.A. MEDLINE=97470991; PubMed=9326634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000953; Chromo.
InterPro; IPR001410; DEAD.
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us-09-761-636a-7.open.rsp

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InterPro; IPR001650; Helicase_C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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STRAIN=Bristol N2;

Matchews P., McMurray A.;

Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Chromatin-remodelling protein that function in vulval cell fate determination.

-!- SUBCELLULAR LOCATION: Nuclear (Potential).

-!- SIMILARITY: Belongs to the SNR2/RAD54 helicase family.

-!- SIMILARITY: Contains 2 PHD-type zinc fingers.

-!- SIMILARITY: Contains 2 chromo domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=20530482; PubMed=11076750;
von Zelewsky T., Palladino F., Brunschwig K., Tobler H., Hajnal A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
0
      PROSITE; PS00690; DEAH ATP HELICASE; 1.
PROSITE; PS01359; ZF PHD 1; 1.
PROSITE; PS01359; ZF PHD 2; 1.
DNA-binding; ATP-binding; Helicase; Nuclear protein; Repeat;
Transcription regulation; Activator; Antigen; Zinc-finger.
ZN FING 35 PHD-TYPE.
DOMAIN 84 156 CHROMO 1.
DOMAIN 179 240 CHROMO 2.
DOMAIN 179 299 ATP (POTENTIAL).
SITE 409 412 DEAH BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHDD_CAEEL STANDARD; PRT; 1787 AA.
Q22516; Q18794;
15-UUL-1999 (Rel. 38, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Chromodomain helicase-DNA-binding protein 3 homolog (CHD-3)
                                                                                                                                                                                                                                                                                                                                                                                                                  60.7%; Score 37; DB 1; Length 892; 60.0%; Pred. No. 52; 2; Indels :ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                         517 V -> I (IN REF. 4).
103021 MW; E11DF7F65A1F6D6D CRC64;
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EMBL; Z67884; CAA91810.1; --
EMBL; Z67881; CAA91810.1; JOINED.
EMBL; Z67881; CAA91798.1; --
EMBL; Z67884; CAA91798.1; JOINED.
PIR; T20160, T20160
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InterPro; IPR001953; Chromo.
InterPro; IPR001410; DEAD.
InterPro; IPR002464; DEAH_box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Caenorhabditis elegans.
                                                                                                                                                                                                                                 240
299
412
617
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                                                                                                                                                                                                    84 11 179 2 292 2 409 4 617 6 892 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                  SITE
CONFLICT
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InterPro; IPR0000330; SNF2 N.

InterPro; IPR001965; Znf_PhD.

InterPro; IPR001965; Znf_PhD.

InterPro; IPR001965; Znf_PhD.

InterPro; IPR001965; Znf_PhD.

InterPro; IPR001841; Znf_Ting.

Pfam; PF00271; helicase_C; 1.

R Pfam; PF00271; helicase_C; 1.

R RART; SM00499; PHD; 2.

R SNART; SM00499; PHD; 2.

R SNART; SM00499; PHD; 2.

R SNART; SM00199; PHD; 2.

R RART; SM00199; PHD; 2.

R ROSITE; PS00199; DEAPH ATP HELICASE; 1.

R RROSITE; PS00199; DEAPH ATP HELICASE; 1.

R RROSITE; RS0016; ZF PHD 1; 2.

R RROSITE; RS0016; ZF PHD 1; 2.
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STRAIN=CBS 340.81 / UVM 4-40;
STRAIN=CBS 340.81 PubMed=9178005;
Vaillancourt L.J., Raudaskoski M., Specht C.A., Raper C.A.;
Vaillancourt L.J., Raudaskoski M., Specht C.A., Raper C.A.;
Fullitiple genes encoding pheromones and a pheromone receptor define the B beta 1 mating-type socificity in Schizophyllum commune.";
Genetics 146:541-551(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schizophyllum commune (Bracket fungus).
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Schizophyllaceae; Schizophyllum.
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ATP (POTENTIAL).
DEAH BOX.
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15-JTL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Mating-type pheromone BBP1(2) precursor.
BBP1(2)
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PHD-TYPE 2.
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Prenylation; Lipoprotein; Pheromone.
PROPEP 1 ? POTENTIAL.
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1787 AA;
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P78743;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A putative chemoattractant receptor, C5L2 is expressed in granulocyte and immature dendritic cells, but mature dendritic cells."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                        Gaps
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"The orphan receptor CSL2 has high affinity binding sites for complement fragments C5a and C5a des Arg(74).";
J. Biol. Chem. 277:1165-7169(2002).

-!- FUNCTION: Receptor for the Chemotactic and inflammatory peptide anaphylatoxin C5a, C4a and C3a and their des arginated derivatives. Couples weakly to Gi-mediated signaling pathways.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUB SPECIFICITY: Frontal cortex, hippocampus, hypothalamus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                      REMOVED IN MATURE FORM (POTENTIAL). S-farnesyl cysteine (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [2]
SEQUENCE FROM N.A.
MEDLINE=21105913; PubMed=11165367;
Lee D.K., George S.R., Cheng R., Nguyen T., Liu Y., Brown M.,
Lynch K.R., O'Dowd B.F.;
"Identification of four novel human G protein-coupled receptors
"Identification of four novel human G protein-coupled receptors
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0
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Ohno M., Hirata T., Enomoto M., Araki T., Sato K., Ishimaru H.,
Takahashi T.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kopatz S.A., Aronstam R.S., Sharma S.V., "cDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org)."; Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
     MATING-TYPE PHEROMONE BBP1(2)
                                                                                   Score 36; DB 1; Length 65;
Pred. No. 4.8;
0; Mismatches 3; Indels
                                   S-farnesyl cysteine (Pot 3341013317AD6065 CRC64;
                                                                                                                                                                                                                                                                                          (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                    337 AA.
                                                                                                                                                                                                                                                                                                                                           C5a anaphylatoxin chemotactic receptor C5L2
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 62
65
62
6780 MW;
                                                                                 59.0%;
                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                               SAPLTEAPC 50
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?
63
62
65 AA;
                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                            GPR77 OR CSL2
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                                                                                                                                                                                                                                                                                             28-FEB-2003
28-FEB-2003
                                                                                                                                                                                                                                                                                                                              15-MAR-2004
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                                               SEQUENCE
                                                                              Query Match
                                                                                                  Local
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HUMAN
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                                                                       Genew; HGNC:4527; GER77.
GO; GO:0016526; F:G-protein coupled receptor activity, unknow. . .; NAS.
InterPro; IPRO0276; GPRR.Rhoddpsn.
Pfam; PF00001; 7tm.1, 1.
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STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE-96337999; Pubmed-8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness B.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nauyen D., Vittenback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C., "Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --- CATALYTIC ACTIVITY: ATP + L-lysine + tRNA(Lys) = AMP + diphosphate + L-lysyl-tRNA(Lys).
--- SUBCELLULAR LOCATION: Cytoplasmic.
--- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
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15-UUL-1998 (Rel. 36, Last sequence update)
28-FSFB-2003 (Rel. 41, Last annocation update)
Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA ligase) (LysRS).
LYSS OR MJO539.
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N-LINKED (GLCNAC. ) (POTENTIAL)
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                                                                                                                                                      PFam; PF00001; / Lum_1, GEGRAHDODSN.
PRINTS; PR00237; GFORENDEN FECEP F1 1; FALSE_NEG.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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Archaea; Buryarchaeota; Methanococci; Methanococales;
Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                           3 (POTENTIAL), CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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4; Mismatches
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        AB038237; BAA95414.1; -. AF317655; AAK12640.1; -.
                                              EMBL; AY268430; AAP23197.1; -.
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EMBL; AB038237; BAA95414.1;
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72
95
1114
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149
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84 CLSLPILAVP 93
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Matches 5; Conserv
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057959;
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SYK_METJA
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 97:14224-14228(2000).

-!- CATALYTIC ACTIVITY: ATP + L-1ysine + tRNA(Lys) = AMP + diphosphate + L-1ysyl-tRNA(Lys).

-!- SUBCELLULAR LOATION: Cytoplasmic.

-!- MISCELLANBOUS: Able to charge E.coli tRNA(Lys) in vitro.

-!- MISCELLANBOUS: Able to charge E.coli tRNA(Lys) in vitro.
                                                                                                                                                            HAMAP; MF 0017; -; 1.

HAMAP; MF 00177; -; 1.

InterPro; IPR002904; LNA-synt lc.

InterPro; IPR001925; LNA-synt bind.

InterPro; IPR001412; LNA-synt I:

Pfam; PF01921; LRNA-synt If; 1.

PTGRFAM; TIGRO0467; Jy8S_arch; 1.

PROSITE; PS00178; AA TRNA LIGASE I; 1.

Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA ligase) (LysRS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ibba M., Morgan S., Curnow A.W., Pridmore D.R., Vothknecht U.C., Gardher W., Lin W., Woese C.R., Soell D.; "A euryarchaeal lysyl-tRNA synthetase: resemblance to class I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20570460; PubMed=11121028; Soell D., Becker H.D., Plateau P., Blanquet S., Ibba M.; "Context-dependent anticodon recognition by class I lysyl-tRNA synchetases.";
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                                                                                                                                                                                                                                                                                                                    "HIGH" REGION.
"KMSKS" REGION.
5811837C8A349E9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Methanococcus maripaludis.
Archaea; Euryarchaeota; Methanococci; Methanococcales;
Methanococcaceae; Methanococcus.
NCBI_TaxID=39152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF 1-22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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MEDLINE=98016282; PubMed=9353192;
                                                                                                                                                                                                                                                                                                                                        278 282 "J
530 AA; 61921 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 278:1119-1122(1997)
                                                                                                                               EMBL; U67503; AAB98532.1; -.
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Best Local Similarity 50.0
Matches 5; Conservative
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84 IGMPLSEIPC 93
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030522;
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DR PRBL; AF009824; AAB87410.1; -.

DR PIR; T46975; T46975.

DR HAMAP; MF 00177: -: 1.

DR InterPro; IPR002904; Lys_tRNA-synt 1c.

DR InterPro; IPR002904; Lys_tRNA-synt bind.

DR InterPro; IPR001412; tRNA-synt li.

DR Ffan; PF001921; tRNA-synt li.

DR Ffan; PF001921; tRNA-synt li.

DR FAMIDACYL-TRNA-synt li.

DR TIGRAMS; TIGRO0467; lys_arch; li.

ET SITE 278 282 "KMSKS" REGION.

FT SITE 278 282 "KMSKS" REGION.

FT SITE 278 282 "KMSKS" REGION.

FT CONFLICT 1 1 -> L (IN REF. 1; AA SEQUENCE).

SQ SEQUENCE 533 AA; 61273 MW; 007FA868A57A0AC2 CRC64;

Acches 5; Conservative 3; Mismatches 2; Indels 0; Gaps

Qy 2 ISVELTSVPC 11

B4 IGMPLSEIPC 93

Search completed: September 5, 2004, 09:56:04

Job time: 7 Secs
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us-09-761-636a-7.open.rspt

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09py69 soybean mos
07u7p2 synechococc
07v6t2 prochloroco
08na51 homo sapien
09xqq5 oryza sativ
08bw61 mus musculu
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Q91ze4 rattus norv
Q9qub7 caenorhabdi
Q8c7w1 mus musculu
Q9nf93 leishmania
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Q8vdf2 mus musculu
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                                                        September 5, 2004, 09:46:09; Search time 24.8889 Seconds (without alignments) 139.448 Million cell updates/sec
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                                                                                                                                                                                            1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                   1017041 seqs, 315518202 residues
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                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
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Q9Z1H6
Q9Y9B5
Q9PY69
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Q8QGD7
Q91ZE4
Q9GUB7
Q8C7W1
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Q7V6T2
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Q8BW61
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sp_bacteria:*
sp_bacteria:*
sp_tung1:*
sp_human:*
sp_mammal:*
sp_mcammal:*
sp_organe1e:*
sp_organe1e:*
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sp_unclassified:*
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sp_rodent:*
sp_virus:*
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                                                                                                                 1 CISVPLTSVPC 11
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Match Length DB
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11111110987651
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m	Ognsw2 homo sapien Ogedw6 homo sapien	Qanava schizosacch Q7t3k0 oncorbynchu	009411 arthroderma	Q68691 hepatitis c	016608 caenorhabdi	Wel424 arabidopsis		α			OBOGHA MESCULA	- (			Conting Craucapoilu		OBOCIA himan ochon				Sample synechococo		O87325 June 10roco	Ve/zus neurospora Q93yrz arabidopsis	
Q8BW83 Q8HXK6	096QW6	Q7T3K0	009411	068691	016608	081291	020852	Q9FYQ8	O7ZUF5	<b>08C7F9</b>	Q8C6H4	019815	OSIF84	6NIN80	09L5F5	9WXS60	080GI4	0908NB	090913	080706	O7XVB5	07VB14	0872N5	Q93YR2	ALIGNMENTS
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737	1411	91	207	318	425	577	616	659	658	662	662	1829	54	105	178	184	191	251	251	272	347	377	389	401	
63.9	63.69		62.3	5.5			62.3	62.3	62.3	62.3	62.3	62.3	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	
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### LL GNMEN

RESULT 1

AC 09GLX1

D 09GLX1

AC 09GLX1

AC 09GLX1

D 1-JUNA-2001 (TrEMBLrel. 16, Created)

D 1-JUNA-2001 (TrEMBLrel. 16, Last sequence update)

D 1-JUN-2003 (TrEMBLrel. 16, Last sequence update)

D 1-JUN-2003 (TrEMBLrel. 14, Last amortation update)

B Vascular endothelial growth factor-D (Fragment).

S Bos taurus (Bovine).

C Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

OX NCBI TaxID-9913;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUB-Lung;

RA Mandriota S.J., Pepper M.S.;

RL Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.

R Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.

BR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0018121; P:cell growth factor activity; IEA.

CO; GO:0018121; P:cell growth factor activity; IEA.

DR GO; GO:0018121; P:cell growth factor:

DR InterPro; IPRO0072; PD_growth_factor:

DR TO; GO:001812; P:cell growth_factor:

R TONN TER 122 122

SC GO:001812; P:cell growth_factor:

R TONN TER 122 122

SC SEQUENCE 122 AA; 13820 MW; CC504B00E29D54BB CRC64;

Query Match

Best Local Similarity 100.0%; Pred. No. 3.5;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps

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2 ISVPLTSVP 10 |||||||||| 1 ISVPLTSVP 9

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SEQUENCE
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                                                                                                                                                                               Q9GUB7;
                                                                                                                                                                   Q9GUB7
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Q9GUB7
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A Kirkin V., Mazitschek R., Krishnan J., Steffen A., Waltenberger J.,

Kirkin V., Mazitschek R., Sleeman J.P.;

Kirkin V., Mazitschek R., Sleeman J.P.;

Kirkin V., Mazitschek R., Sleeman J.P.;

Pepper M.S., Giannis A., Sleeman J.P.;

Pepper M.S., Giannis A., Sleeman J.P.;

REAT-Carcerization of indolinones which specifically inhibit VEGF-C-and

VEGF-D-induced activation of VEGFR-3 but not VEGFR-2.";

REMBL, AN012728; AAK96008.1;

REMBL, AN012728; AAK96008.1;

ROJ, GO:0008083; F:Growth factor activity; IEA.

GO; GO:0008151; P:Cell growth and/or maintenance; IEA.

ROJ, GO:0008151; P:Cell growth and/or maintenance; IEA.

RITHERPO; IPRO04153; CXCXC repeat.

RITHERPO; IPRO0415; PD growth_factor.

REAM: PROD041; PDGF; 1.

REAM: PROD041; PDGF; 1.
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                                                                                                                                                                                               biaz-Trelles R., Rodriguez-Leon J., Kawakami Y.,

Diaz-Trelles R., Rodriguez-Leon J., Kawakami Y.,

Izpisua-Belmonte J.C.;

Izpisua-Belmonte J.C.;

during limb development.";

Mech. Dev. 0:0-0(2002)

REMEL; AF479550; AAM12733.1;

ROJ GO:0016020; C:membrane; IEA.

ROJ GO:0016020; C:membrane; IEA.

ROJ GO:0008151; P:cell growth factor activity; IEA.

ROJ GO:0008151; P:cell growth factor.

R Pfam; PF00341; PDGF; PD_growth_factor.

R Probom; PD001629; PD_Growth_factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                               Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
                                                                                                                                                                                                                                                                                                                                                                                                                                70.5%; Score 43; DB 13; Length 252; 100.0%; Pred. No. 7.1; o; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
SEQUENCE 252 AA; 28767 MW; 643475DAB2E72F27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q91ZE4;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                01-UTN-2002 (TrEMBLrel. 21, Created)
01-UTN-2002 (TrEMBLrel. 21, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Vascular endothelial growth factor D.
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                        252 AA
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                        PRT;
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Matches 9; Conservative
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                         PRELIMINARY;
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SEQUENCE FROM N.A.
                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                              NCBI TaxID=9031;
                                         Q8QGD7;
01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                           080GD7
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Q91ZE4
RESULT 2
Q8QGD7
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Direct Submission."; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. BEMBL; AR078157; ARG24081.1; -... WormPep; F25E5.13; EC24915. GO; GO:0016020; C:membrane; IEA. GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 54.5%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 3; Indels
                                                                70.5%; Score 43; DB 11; Length 326; 100.0%; Pred. No. 9.1; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Bristol N2; wilson R., Bradshaw H.; Wilson R., Bradshaw H.; "The sequence of C. elegans cosmid F25E5."; Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39882 MW; 456DEC8833CF3176 CRC64;
PROSITE; PS50278; PDGF 2; 1.
SEQUENCE 326 Aa; 37106 MW; D7CAEBA6C9FABB7D CRC64;
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Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003003, 7TM chemrecept2.
InterPro; IPR000168; Nm/TM chemrecept2.
Pfam; PF01604; 7tm 5; 1.
Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                 PRT;
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STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, C)
01-MAR-2001 (TrEMBLrel. 16, Li
01-OCT-2003 (TrEMBLrel. 25, Li
Hypothetical protein.
F25E5.13.
Caenorhabditis elegans.
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                                                      Query Match
Best Local Similarity 100..

Best Local Similarity 100..
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                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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348 AA; 39
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                                                                                                                                                                      2 ISVPLTSVP 10
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Ranari Y., Kubo E., Kurihara T., Takabe T., Tatsumi K., Muto M.;

Ranari Y., Kubo E., Kurihara T., Takabe T., Tatsumi K., Muto M.;

"Targeted Disruption of Mp55 Gene Renders ES cells Hypersensitive to
"Targeted Disruption of Mp55 Gene Renders ES cells Hypersensitive to
"Targeted Disruption of Mp55 Gene Renders ES cells Hypersensitive to
"E Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

E Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

"E Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

"E GO GO:000547; F:DNA binding; IEA.

"GO; GO:000547; F:DNA binding; IEA.

"GO; GO:0006355; F:regulation of transcription, DNA-dependent; IEA.

"
                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC02167; AH22167.1; -.
MCD; MCJ:1338B89; NpS5.
GO; GO:0005515; F:transporter activity; IEA.
GO; GO:0005515; P:transporter activity; IEA.
GO; GO:0006810; P:transporter activity; IEA.
InterPro; DR001056; Lipocln cytFABP.
InterPro; IPR000566; Lipocln cytFABP.
InterPro; IPR000565; Znf_PHD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Sukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.6%; Score 40; DB 11; Length 474; 70.0%; Pred. No. 46; 2; Indels iive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          474 AA; 53685 MW; OEAE841CCD8C7FEA CRC64;
                                  01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
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01-MAR-2002 (TrEMBLrel. 20, Last seq
01-0CT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00213; LIPCALIN; 1.
PROSITE; PS0053; UBIQUITIN_2; 1.
PROSITE; PS01359; ZF PHD 1; 1.
PROSITE; PS50016; ZF PHD 2; 1.
PROSITE; PS50089; ZF RING_2; 1.
NON_TER
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Matches 7; Conservative
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                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                            NCBI_TaxID=10090;
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                                                             Np95 (Fragment).
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SEQUENCE
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Q8VDF2
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                                                                                                                                                                                              The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:663-573 (2002).
EMBL; AK049158; BAC33576.1; ...
MGD; MGT:2147036; C330008L01Rik.
Hypothetical protein.
SEQUENCE 118 AA; 12658 MW; 7245EA4643F9123A CRC64;
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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SEQUENCE FROM N.A.
STRAIN-Friedlin;
Ivens A.C., Murphy L., Quail M., Harris D., Oliver K., Lawson D.,
Rajandream M.A., Barrell B.G.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=98146435; PubMed=9477341;
Lvens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
Smith D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A physical map of the Leishmania major Friedlin genome.";
Genome Res. 8:135-145(1998).
BML1; AL139794; CAC22646.1; -.
GO; CO16021; C:integral to membrane; IEA.
Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical transmembrane protein L8032.05a.
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Last sequence update)
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                                                                                                                                                      STRAIN=CS7BL/6J;
MEDLINE=22354683; PubMed=12466851;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 CLPTPLTPTPC 105
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Best Local Similarity 63.6
Matches 7; Conservative
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QBVIA1;
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Q9NF93

RESULT 6
20NF93
1D 00NFP
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DT 01-0
DE HYPO
GN Leis3
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QBVIA1 ID QE AC QE DT 0: DT 0:

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Query Match 63.9
Best Local Similarity 60.0
Matches 6; Conservative
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                349 CLKPPLTSVP 358
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NCBI_TaxID=12222;
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SQUENCE FROM N.A.
BAGUENCE FROM N.A.
Davenport J.W., Fernandes B.R., Neale G.A.M., Goorha R.M.;
Davenport J.W., Fernandes B.R., Neale G.A.M., Goorha R.M.;
FING-induced T cell leukemias overexpress Np55, a gene containing
RING and PHD zinc fingers and an ubiquitin-like domain.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; BA74908; BAA74579.1;
EMBL; AF274046; AAK55743.1;
HSSP; Q15843; INDD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Nuclear protein np95 (Nuclear zinc finger protein Np95).
Mus musculus (NRF).
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musl.
11 TaxID=10090;
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PROSITE; PSG0053; UBIQUITIN_2; 1.
PROSITE; PSG0053; ZF_PHD_1; 1.
PROSITE; PSG00159; ZF_PHD_2; 1.
PROSITE; PSG00818; ZF_RING_1; 1.
PROSITE; PSG0089; ZF_RING_2; 2.
SEQUENCE 782 AA; 88319 WW; DCSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Pre-Tcell;
MEDLINE=99099250; PubMed=9880673;
                      Pfam; PF00628; PHD; 1.
Pfam; PF00240; ubiquitin; 1.
Pfam; PF00240; vbiquitin; 1.
Pfam; PF00197; zf-C3HC4; 1.
PRINTS; PR00348; UBIQUITIN.
SMART; SM00249; PHD; 1.
SMART; SM00184; RING; 2.
SMART; SM00184; RING; 2.
          InterPro; IPR001841; Znf_ring
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Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPPY69;

OHAY-2000 (TrEMBLrel. 13, Created)

OHAY-2000 (TrEMBLrel. 13, Last sequence update)

OH-UNA-2003 (TrEMBLrel. 24, Last annotation update)

OH-UNA-2003 (TrEMBLrel. 24, Last annotation update)

El procease (Fragment)

Soybean mosaic virus.

Viruses; SSRNA positive-strand viruses, no DNA stage, Potyviridae;
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                                                                                                                                                                                                                                                                                                                                                  Score 40; DB 11; Length 782;
Pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea, Crenarchaeota, Thermoprotei, Desulfurococcales, Desulfurococcaceae, Aeropyrum.
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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DNA Res. 6:83-101(1999).

EMBL; AP000064; BAA81385.1; -.

PIR; A72466; A72466; Complete proteome.

Hypothetical protein; Complete proteome.

SEQUENCE 169 AA; 17432 MW; 9BDB7147C7B1426A CRC64;
                                                                                                                                                                                                                                                                                                 DCSEEDFCDF69619B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein APE2372.
                                                                                                                                                                                                                                                                                                                                                                                                                     5
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SMART; SM00249; PHD; 1.

SMART; SM00184; RING; 2.

SMART; SM00466; SRA; 1.

SMART; SM00213; UBO; 1.

PROSITE; PS00213; LIPOCALIN; 1.

PROSITE; PS01359; ZF PHD 1; 1.

PROSITE; PS01159; ZF PHD 2; 1.

PROSITE; PS01018; ZF RING 1; 1.

PROSITE; PS0018; ZF RING 1; 1.

PROSITE; PS0018; ZF RING 1; 1.

PROSITE; PS20089; ZF RING 1; 1.
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RA TISSUE-TESTIS.

RA Arita M., Musashin-Fujii A., Tanase T., Imose N., Takeuchi K., Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R., Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R., RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamanoto J., Isono Y., Rawai-Hio Y., Saito K., Mishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T., RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T., R. Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

RE Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

BRE: AKO93157; BACO4077.1; --
DR InterPro; IPRO09957; FN_III-
DR InterPro; IPRO08957; FN_III-
DR Ffam; PF00041; fn3; 1.

SMART' SMO0060; FN3; 4.

KW Hypotherical protein.
            MEDINE-22825699; PubMed=12917642;
Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
Ablgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
Obnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M.,
Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
Webb E.A., Zinser E.R., Chisholm S.W.;
"Genome divergence in two Prochlorococcus ecotypes reflects oceanic
niche differentiation.";
Nature 424-11042-1047(2003).
EMBL, BX572099; CAR212371; -
Oxidoreductase; Complete proteome.
SEQUENCE 386 AA; 41291 MW; 2CACG14ACF010B1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                          63.9%; Score 39; DB 16; Length 386; 54.5%; Pred. No. 57; 2; Indels tive 3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                         Indels
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ35838.
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Last annotation update)
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01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-UUN-2003 (TrEMBLrel. 24,
EST8 AU064813(E40579).
                                                                                                                                                                                                                                                                                                                                  6; Conservative
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|22 CITVPLSAATC 132
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Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity
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SEQUENCE FROM N.A.
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ID 059
AC 069
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                                    Latorre 1.7., Domier L.L., Hartman G.L.;
"Natural variability of soybean mosaic virus.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AP200544; AP13954.1; --
GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
GO; GO:0006508; F:peptidase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro: IPR002540; Poty_P1.
Pfam: PF01577; Poty_P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDILINE=22825697; PubMed=12917641;

MEDILINE=22825697; PubMed=12917641;

Palenik B., Barhamsha B., Larimer F.W., Land M., Hauser L., C
Lamerdin J., Regala W., Allen E.E., McCarren J., Paulsen I.,

Dufresne A., Partensky F., Webb E.A., Waterbury J.;

"The genome of a motile marine Synechococcus.";

Nature 424-11037-1042(2003).

EMBL; BX569691; CR67454.1; -.

Oxidoreductase; Complete proteome.

SEQUENCE 366 AA; 38076 MW; 4C9E5230413AA11B CRC64;
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Prochlorococcus marinus (strain MIT 9313).
Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcacea;
                                                                                                                                                                                                                                                                                                                                    63.9%; Score 39; DB 12; Length 318; 70.0%; Pred. No. 48;
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                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
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318 AA; 36291 MW; 0D2C1B46035AEAF1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synechococcus sp. (strain WHB102).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative glycerol dehydrogenase (EC 1.1.1.6).
GLDA OR PMT1062.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Putative glycerol dehydrogenase (EC 1.1.1.6)
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| 113 CITVPLSAATC 123
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NCBL_TaxID=74547;
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01-OCT-2003
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SEQUENCE
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Q7U7P2;

Q7U7P2

RESULT 12 Q7U7P2

Db

Matches

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Query Match

Matches

Q7V6T2;

Q7V6T2

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Gaps

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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae, Oryza.
                                                                                       | I. | SEQUENCE FROM N.A. | SEQUENCE FROM N.A. | STAIN—C. Nipponbare; Sasaki T., Matpundto T., Yamamoto K.; Sasaki T., Matpundto T. | Chone: POOSCEPOT. | Submitted (JUN. 1999) to the EMBL/GenBank/DDBJ databases. | EMBL; AP000364; BAA81763.1; -. | EMBL; AP000364; BAA81763.1; -. | GO; GO: 0016021; C: Integral to membrane; IEA. | GO; GO: 0006215; P: transporter activity; IEA. | GO; GO: 0006810; P: transport. IEA. | R GO; GO: 0006810; P: transport. | IEA. | InterPro; IPR004240; EMP70. | InterPro; IPR004240; EMP70. | InterPro; IPR004240; EMP70. | SEQUENCE 661 AA; 74533 MW; 612242C132F68BEB CRC64;
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Best Local Similarity 88.9%; Pred. No. 96;
Matches 8; Conservative 0; Mismatches 1; Indels
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Search completed: September 5, 2004, 09:59:56 Job time : 26.8889 secs

478 CISVPLTLV 486

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd. Copyright

OM protein - protein search, using sw model

5, 2004, 09:37:49; Search time 36.1111 Seconds (without alignments)
86.068 Million cell updates/sec September Run on:

US-09-761-636A-7 61 1 CISVPLTSVPC 11 Perfect score: Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

1586107 seqs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 DB Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2003as:* A Geneseq 29Jan04:* geneseqp2003bs:* geneseqp2001s:* geneseqp2002s:* geneseqp2004s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		ΔI	AAU04526	AAU04542	AAU04545	AAU04543	AAU04544	AAU04532	AAU04520	AAY23889	AAB11931	ABB84621	17040704	ABG/3/50	AAM4 / 933	AAY08287	ABG73779	AAW53243	AAM47931	AAW53240	AAY97572	AAW44296	AAVOROBE	N N M N N N N N N N N N N N N N N N N N	0.000	AAW49036	AAW53241	AAB10649	AAY70750	
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AAY70983 AAB29049 AAB29049 AAB37606 AAB70685 AAV97573 AAU08411 AAU08441 AAU08441 AAU14992 AAW44295 AAW44295 AAW44295 AAW44294 AAX07909 AAW14994 AAX07909	AAG04076 ABM74219
<b>ww44440006644000000044</b>	7 3 4
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7000 7000 7000 7000 7000 7000 7000 700	65.6
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	144
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	44

## ALIGNMENTS

AAU04526 standard; peptide; 11

AA.

AAU04526;

26-SEP-2001

(first entry)

VEGF based monocyclic peptide 3.

Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.

Synthetic.

/note= "This bond cyclises the peptide" Location/Qualifiers Disulfide-bond

WO200152875-A1 26-JUL-2001.

18-JAN-2001; 2001WO-US001533.

18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P.

Cendron A; Stacker S, (LUDW-) LUDWIG INST CANCER RES. Achen MG, Hughes RA,

WPI; 2001-442248/47.

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues

Claim 49; Page 32; 102pp; English.

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGPD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabeta carbon separation distances on opposite antiparallel strands of a 

residues

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cc peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptides by oxidiaing the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic cc peptides) and a cyclic peptide with at least one amino acid deleted prior cyclisation are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis.

Cc characterised by angiogenesis, neovascularisation or lymphangiogenesis.

The condition is diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised malignant or benign tumour, post-recovery cc crebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid corporateure. The monomeric and bicyclic peptides are used to interfere vasculariation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to modulate vascular permeability or brain. The peptides are used to modulate vascular permeability are least one biological activity induced by VEGF, VEGF-C or D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and chronic inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; VEGF; vascular endothelial growth factor; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 61; DB 4; Length 11; 100.0%; Pred. No. 0.0016; ive 0; Mismatches 0; Indels

    .11
    /note= "This bond cyclises the peptide"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU04542 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEGF based monocyclic peptide 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JAN-2001; 2001WO-US001533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CISVPLTSVPC 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU04542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU04542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
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The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human whose 3-dimensional structure is modelled on the expose loop of human consideration of producing a monomeric monocyclic peptide by a measuring beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and peptides by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenes; to cyclisation are used to interfere with angiogenes; condition are used to interfere with angiogenes; to cyclisation are used to interfere with angiogenes; condition is diabetic retinopathy, psoriasis, arthrogathy. The condition is diabetic retinopathy, psoriasis, arthrogathy, cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive to rememe a substance-induced neovascular sequelae, nypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability cor brain. The peptides are also used to modulate vascular permeability or brain. The peptides are used to image blood vesels and lymphatic cor brain. The peptides are used to image blood vesels and lymphatic cor brain the petides are used to image blood vesels and lymphatic cor brain the last one biological activity induced by VEGF. VEGF. Cor D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 59; DB 4; Length 11;
Pred. No. 0.0034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels

    .11
/note= "This bond cyclises the peptide"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                    Example 25; Page 47; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU04545 standard; peptide; 11 AA
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16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JAN-2001; 2001WO-US001533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CISVPLTSVPC 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU04545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
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The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human verses of vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betacenested loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptide with at least one amino acid deleted prior cyclising the peptide with at least one amino acid deleted prior peptides, and acyclic peptide with at least one amino acid deleted prior cyclisation are used to interfere with angiogenesis.

Comparation are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis, neovascularisation or lymphangiogenesis, neovascularisation or lymphangiogenesis.

Confaraterised by angiogenesis, neovascularisation or lymphangiogenesis.

Confaraterised by angiogenesis, neovascularisation or lymphangiogenesis.

Confaraterised malignant or benign tumour, post-recovery corresponsed by angiogenesis, neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, or chronic liver confirmed in peripheral limbs or in lungs, peritoneal cavity, pleura, infection. The peptides are used to indefere correct or brain. The peptides are used to indefere correct or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or D and care also used in combination with an unit infilmment of contractive and chickle are used to interfere contractive and chickle are used to interfere contractive and chickle are used to interfere contractive and chickle are used to interfere contractive and chickle are used to interfere contractive and contractive and contractive and contractive and contractive and contractive and contractive and contr
                                                                                                                                                                                 Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chronic inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                        Example 25; Page 47; 102pp; English.
(LUDW-) LUDWIG INST CANCER RES.
                                                                Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diabetic retinopathy
                                                                                                                          WPI; 2001-442248/47
                                                                Achen MG,
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Sequence 11 AA;

Gaps .; o Score 57; DB 4; Length 11; Pred. No. 0.0072; 2; Mismatches 0; Indels 9; Conservative Query Match Best Local Similarity Matches

26-SEP-2001 (first entry)

growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic. Human; VEGF; vascular endothelial VEGF based monocyclic peptide 21.

Synthetic.

/note= "This bond cyclises the peptide" Disulfide-bond

1 CVSVPLTTVPC 11 1 CISVPLTSVPC 11 ò

0

AAU04543 standard; peptide; 11 AA. 

Location/Qualifiers

WO200152875-A1

26-JUL-2001

Cendron A;

Stacker S,

18-JAN-2001; 2001WO-US001533

18-JAN-2000; 2000US-0176293P

16-MAY-2000; 2000US-0204590P

(LUDW-) LUDWIG INST CANCER RES

Cendron A; Stacker S, Achen MG, Hughes RA,

WPI; 2001-442248/47.

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.

Example 25; Page 47; 102pp; English.

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human verses and vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betact carbon separation distances on opposite antiparallel strands of a petide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis.

Conversional are used to interfere with angiogenesis.

Converterised by angiogenesis, neovascularisation or lymphangiogenesis.

Converterised by angiogenesis in a mammal with a condition characterised by falling a condition or benign tumour, post-recovery cerebrovascular accident, post-rangioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive correspondent induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid cormulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to inage blood vessels and lymphatic vascularing are used to image blood vessels and lymphatic correct and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and characterised by the condition with an anti-inflammation; to treat a chapter or return of a separatic retunopathy 

Sequence 11 AA;

Score 54; DB 4; Length 11; Pred. No. 0.023; 3; Mismatches 0; Indels 0; Indels 88.5%; 72.7%; Local Similarity 72.7 les 8; Conservative Query Match Matches

.; 0

Gaps

0;

||::|||:|| CITIPLTSLPC 11 1 CISVPLTSVPC 11

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AAU04544 standard; peptide; 11 AA. AAU04544 RESULT

(first entry) 26-SEP-2001

AAU04544;

VEGF based monocyclic peptide 22.

Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; 

Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.

11 /note= "This bond cyclises the peptide"

Location/Qualifiers

VEGF based monocyclic peptide 10.

(first entry)

26-SEP-2001

AAU04532;

1. .10 /note= "This bond cyclises the peptide"

Location/Qualifiers

Key Disulfide-bond

Synthetic.

WO200152875-A1

26-JUL-2001

Cendron A;

Stacker S,

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Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
diabetes induced neovascular sequelae, rheumatoid arthritis; diabetic retinopathy, chronic inflammation; cyclic.
                                                                                                                                                                                                                        Example 25; Page 47; 102pp; English.
                                                                                                                                        (LUDW-) LUDWIG INST CANCER RES
                                                                                                                         16-MAY-2000; 2000US-0204590P.
                                                                                                  18-JAN-2001; 2001WO-US001533
                                                                                                                  18-JAN-2000; 2000US-0176293P
                                                                                                                                                       Hughes RA,
                                                                                                                                                                     WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11 AA;
                                              Disulfide-bond
                                                                      WO200152875-A1
                                                                                     26-JUL-2001
                         Synthetic
                                                                                                                                                       Achen MG,
                                                                                                                                                                                                           residues.
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Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine

Claim 49; Page 32; 102pp; English.

residues.

Cendron A;

Stacker S,

Hughes RA,

Achen MG,

WPI; 2001-442248/47.

(LUDW-) LUDWIG INST CANCER RES 16-MAY-2000; 2000US-0204590P.

18-JAN-2001; 2001WO-US001533. 18-JAN-2000; 2000US-0176293P

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The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human to whose 3-dimensional structure is modelled on the expose loop of human correction to a sequence of producing a monomeric monocyclic peptide by a measuring beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis.

The condition is lymphangiogenesis in a mammal with a condition controlled by angiogenesis, neovascularisation or lymphangiogenesis.

The condition is diabetic retinopathy, psoriasis, arthropathy correspondance in the condition and adjabetic retinopathy, psoriasis, arthropathy correspondance creabrovascular accident, post-angioplasty restenosis, head, heat or cold crauma, substance-induced meovascularisation of the liver, excessive creamma, substance-induced neovascular sequelae, or chronic liver, infartion the maniformal or maniformal accident maniformal and sequence induced neovascular sequelae, or chronic liver, infartion the maniformal and condition induced neovascular sequelae, and condition induced neovascular sequelae, or chronic liver, infartion when prevides a condition induced neovascular sequelae, and condition induced neovascular sequelae, and condition induced neovascular sequelae, and condition induced neovascular sequelae, and condition induced neovascular sequelae, or chronic liver, infartion when prevides and conditions and co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human whose 3-dimensional structure is modelled on the expose loop of human vegoe 0 to according to the peptide by a measuring beta-cc peptide of producing a monomeric monocyclic peptide by a measuring beta-cc peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cyclein and exposed loop of a growth factor protein and cyclisation are used to interfere with angiogenes; The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior cyclisation are used to interfere with angiogenes; to cyclisation are used to interfere with angiogenes; to cyclisation are used to interfere with angiogenes; to cyclisation is diabetic retinopathy, psoriaasis, atthropathy. The condition is diabetic retinopathy, psoriaasis, atthropathy, cerebrovascular accident, post-angioplasty restenosis, head, heat or condition is diabetic retinopathy, psoriaasis, atthropathy. Corebrovascular accident, post-angioplasty restenosis, head, heat or chromon-related angiogenic dysfunction, diabetes induced neovascular sequelae, nypertension induced neovascular sequelae, or chromic liver commandal has are also used to modulate vascular permeability corbrain. The peptides are used to image blood vesels and lymphatic corbrain. The peptides are used to image blood vesels and lymphatic corbrain are least one biological activity induced by VEGF. VEGF-C or b and are also used in combination with an anti-inflammatory agent, to treat a chromic inflammation, especially rheumatoid arthritis, psoriasis and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 Similarity 90.9%;
10; Conservative
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AAU04532 standard; peptide; 10 AA.

RESULT 6 AAU04532 ID AAU04

|||:|::|||| 1 CISLPISSVPC 11

Best Loc Matches

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CISVPLTSVPC 11

(first entry)

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The sequence represents Human VEGF-D (vascular endothelial growth factor)

a mino acids val101-PR0186. The sequence is used in a method of producing

a monomeric monocyclic peptide by a measuring beta-beta carbon separation

distances on opposite antiparallel strands of a peptide loop fragment

from an exposed loop of a growth factor protein and cyclising the peptide

c by oxidising the cysteine residues. The monocyclic peptides, dimeric

bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic

peptide with at least one amino acid deleted prior to cyclisation are

lymphangiogenesis in a mammal with a condition or lymphangiogenesis. The condition is

angiogenesis, neovascularisation or lymphangiogenesis. The condition is

angiogenesis, neovascularisation or lymphangiogenesis. The condition is

malignant or benigh tumour, post-recovery cerebrovascular accident, post-

neovascularisation of the liver, excessive hormone-related angiogenic

dysfunction, diabetes induced neovascular sequelae, hypertension induced

neovascular sequelae, or chronic liver infection. The peptides are also

condition characterised by fluid accumulation in peripheral limbs or in

lunds. Derithoneal cavity. When the mammal has a

condition characterised by fluid accumulation in peripheral limbs or in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lungs, peritoneal cavity, pleura, or brain. The peptides are used to mage blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF. VEGF.C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy
                                                                                                                                                                                                                                                                                                         Human; VEGF-D; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriaeis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation.
                                                                                                                                                                                                                                                                  Human VEGF-D amino acids Val101-PRO186.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 89; 102pp; English.
                                                                                                                                       AAU04520 standard; protein; 96 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JAN-2001; 2001WO-US001533
                       WPI; 2001-442248/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 96 AA;
                                                                                                                                                                                                                           26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUL-2001.
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                                                                                                                                                                                  AAU04520;
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Cendron A;

Stacker S,

Hughes RA,

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The present sequence represents human vascular endothelial growth factor (VEGF)-D. The specification describes a human cell line which stably corpresses VEGF-D, or fragments/analogues having VEGF-D biological activity. VEGF-D antagonists, e.g. antisense nucleic acids or triplex activity. VEGF-D antagonists, e.g. antisense nucleic acids or triplex DNA, VEGF-D variants or antibodies (especially chimeric antibodies), are useful for the treatment or alleviation of malignant melanomas, tumours or psoriasis. Angiogenesis and lymphangiogenesis stimulating amounts of vEGF-D can be administered to enhance the acceptance and/or healing of skin grafts or to stimulate the healing of a surgical or traumatic wound to treat lymphagiogenesis stimulating amounts of VEGF-D are used to treat schmilating amounts of vEGF-D are used to treat anhydrotic ectodermal dysplasia. VEGF-D antibodies are useful for detecting tumours expressing VEGF-D. Fully-Corposesed VEGF-D can be used to stimulate at least one VEGF-D. Fully-Corposes of VEGF-D can be used to stimulate at least one VEGF-D. Fully-Corposes of VEGF-D can be used to stimulate at least one VEGF-D. Fully-Corposes of VEGF-D can be used to stimulate at least one VEGF-D bioactivity differentiation and lymphangiogenesis without inducing vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A human cell line stably expressing vascular endothelial growth factor D, useful for treating melanomas or tumors expressing VEGF-D.
                                                                                                                                                                                                                                                                                                                             Vascular endothelial growth factor; VEGF; VEGF-D; malignant melanoma;
tumour; psoriasis; anglogenesis; lymphanglogenesis; skin graft;
wound healing; lymphedema; scleroderma; anhydrotic ectodermal dysplasia.
                                         Gaps
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     Length 96;
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                                       0; Indels
                                                                                                                                                                                                                                                                                            Human vascular endothelial growth factor (VEGF)-D.
   4
            100.0%; Prea. ....
 70.5%; Score 43; 100.0%; Pred. No.
                                                                                                                                                                                        AAY23889 standard; protein; 109 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alitalo K;
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100.0%; Pre-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0087392P.
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                                                                                                                                                                                                                                                             21-SEP-1999 (first entry)
                Similarity 100.
9; Conservative
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                                                                      2 ISVPLTSVP 10
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                                                                                                     ISVPLTSVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9933485-A1.
                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-DEC-1997;
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Query Match
Best Local S:
Matches 9
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                                                                                                                                                                                                                           AAY23889;
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84

AAB1193

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Human; single-chain; extracellular ligand-binding domain; VEGF;
vascular endothelial growth factor; VEGF type 2 receptor; KDR; Flt-4;
VEGF type 3 receptor; VEGF-C; VEGF-D; signal transduction; angiogenesis;
                                                                                                                                                  Human wild-type VEGF-D monomer SEQ ID 3.
ABB84621 standard; protein; 109 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-APR-2001; 2001DK-00000578.
06-APR-2001; 2001US-0282239P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-APR-2002; 2002WO-DK000233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference 60
                                                                                                                                                                                                                                                                                          lymphangiogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200281520-A2
                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                        01-APR-2003
                                                        ABB84621;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
     This sequence represents a 109 amino acid truncated human VEGF-D (Vascular endothelial growth factor D), lacking both the N- and C- terminal regions. The invention relates to a monoclonal antibody, or fragments thereof, which is specifically reactive with the truncated human VEGF-D, and methods of preparing the antibody. The antibody of the invention interferes with the binding of VEGF-D to the VEGF receptors (VEGF-Z) and additionally is not reactive with VEGF-C. The these receptors and additionally is not reactive with VEGF-C. The antibody may be used to treat disorders associated with vascular permeability, endothelial cell proliferation, anglogenesis, lawbeard and endothelial cell (ifferentiation, especially cancer, diabetic retinopathy, psecially cancer, diabetic retinopathy, psecially cancer, diabetic retinopathy, psecially and may also be used to treat fluid accumulation in the heart and/or lung via modulation of vascular permeability. It may in the heart and/or lung via modulation of vascular permeability. It may and the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel compositions comprising antibodies reactive to vascular endothelial growth factor-D, useful for treating, e.g. angiogenesis, lymphogiogenesis and neovascularization disorders.
                                                                                                                                                                                                                                                                                                                  Truncated VEGF-D; vascular endothelial growth factor; human; monoclonal antibody; VEGF receptor; VEGFR-2; VEGFR-3; vascular permeability disorder; endothelial cell proliferative disorder; angiogenic disorder; hymphangiogenic disorder; meovascularisation disorder; endothelial cell differentiation disorder; cancer; diabetic retinopathy; psoriasis; arthropathy; pulmonary oedema; detection; diagnosis; imaging; lymphatic vasculature.
                                                                                                                     AAB11931 standard; protein; 109 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 1; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US031332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0113254P.
99US-0134556P.
                                                                                                                                                                                                                          20-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                          Human truncated VEGF-D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Achen MG, Stacker SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vasculature in tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-442498/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 109 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JUN-2000
                                                                                                                                                                          AAB11931;
                                                                        RESULT 9
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as Gln in Claim 9"

/note= "region of monomer likely to be modified by mutation as described in claim 9"

'note= "This residues is described

98.

/note= "region of monomer likely to be modified by mutation as described in claim 9" /note= "region of monomer likely to be modified by mutation as described in claim 9"

55. .60

monomer likely to be modified by

/note= "region of monomer likely mutation as described in claim 9"

Location/Qualifiers

8. .18 /note=

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This invention describes a novel single-chain dimeric polypeptide which binds to extracellular ligand-binding domain of vascular endothelial binds to extracellular ligand-binding domain of vascular endothelial comparison to the polypeptide of the invention comprises two receptor-binding sites of which one is capable of binding to a ligand-binding domain of the receptor, and at least one monomer of the dimeric domain of the receptor, and at least one monomer of the dimeric polypeptide is derived from VEGF. Or VEGF-C or VEGF-D, where the polypeptide of the invention is useful for preparing a medicament for preventing or treating a disease or condition involving increased signal transduction from, or an increased activation of a VEGF increased signal transduction from, or an increased activation of a VEGF increased signal transduction from, or an increased activation of a VEGF increased signal transduction from, or an increased activation of a VEGF increased signal transduction from, or an increased activation of a VEGF increased such and an increased schain vEGF increased which can be modified and used in the construction of a VEGF-D assed KDR antagonist described in the disclosure of the invention
Novel single-chain dimeric polypeptide for inhibiting angiogenesis, bite extracellular ligand-binding domain of vascular endothelial growth factor type 2/type 3 receptor but does not activate the receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6; Length 109;
16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43;
Pred. No.
                                                                                                                                                                                                                         Claim 9; Page 66; 71pp; English.
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100.0%;
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Best Local Similarity
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Gaps 0;

70.5%; Score 43; DB 3; Length 109; 100.0%; Pred. No. 16; ive 0; Mismatches 0; Indels

9; Conservative

Matches

Query Match Best Local Similarity

2 ISVPLTSVP 10

84

76 ISVPLTSVP

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RESULT 10 ABB84621

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WPI; 2003-058505/05.
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 109 AA;
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        ·,
                                                                                                                                                                                                                                                                                                  /note= "This wild-type residue is replaced by Arg or Glu in the first monomer unit of the VEGF-D dimer if the E57R mutation has not occurred (see Claim 16) and is optionally replaced if the E57R mutation has occurred. The claim describes this residue as Ser but is shown as if in the sequence listing"
                                                                                                                                                                                                                                                                                                                                                                              /note= "This wild-type Asn residue is optionally replaced
by Arg in the second monomer unit of the VEGF-D dimer
(See Claim 11)"
                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "This wild type Thr residue is optionally replaced by Arg or Glu in the second monomer unit of the VEGF-D dimer (see Claims 11 and 16)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "This wild type Phe residue is optionally replaced by Arg or Glu in the second monomer unit of the VEGF-D dimer (see Claims 11 and 16)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "This wild type Phe residue is optionally replaced by Arg in the second monomer unit of the VEGF-D dimer (see Claim 11)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "This wild type lle residue is optionally replaced by Arg or Glu in the second monomer unit of the VEGF-D dimer (see Claim 16)"
                                                                                                                                                                                     Human; single-chain, extracellular ligand-binding domain; VEGF;
vascular endothelial growth factor; VEGF type 2 receptor; KDR; Flt-4;
VEGF type 3 receptor; VEGF-C; VEGF-D; signal transduction; angiogenesis;
lymphangiogenesis; mutant; mutein; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Wild type Gln is replaced by Arg in the first monomer unit of the VEGF-D dimer (See Claim 11) and is optionally replaced if the S10R/E mutation has occurred (see Claim 16)"
        Gaps
        ò
      Indels
     .
   Mismatches
                                                                                                                                                               Human VEGF-D monomer unit E57R variant.
                                                                                              ABG73750 standard; protein; 109 AA.
                                                                                                                                                                                                                                                                               Location/Qualifiers
   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-APR-2001; 2001DK-00000578.
06-APR-2001; 2001US-0282239P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'label= E57R
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                                                                                                                                            (first entry)
 9; Conservative
                     2 ISVPLTSVP 10
                                         76 ISVPLTSVP 84
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                                                                                                                                                                                                                                                        Synthetic
                                                                                                                     ABG73750
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Matches
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This invention describes a novel single-chain dimeric polypeptide which binds to extracellular ligand-binding domain of vascular endothelial and stock to extracellular ligand-binding domain of vascular endothelial and sycopy the factor (VBGF) type 2 receptor (KDR) or VBGF type 3 receptor (Rlt-C of which one is capable of binding to a ligand-binding domain of the receptor, and at least one monomer of the dimeric comain of the receptor, and at least one monomer of the dimeric comparable of binding to the receptor, but incapable of activating the medicament for breyenting or treating a disease or condition involving increased signal transduction from, or an increased activating the medicament for preventing or treating a disease or condition involving type 2 or type 3 receptor e.g. for inhibiting angiogenesis or receptor increased signal transduction from, or an increased activation of a VBGF cype 2 or type 3 receptor e.g. for inhibiting angiogenesis or fype 2 or type 3 receptor e.g. for inhibiting angiogenesis. This sequence represents a variant of the human VBGF-D (STAPPA and optionally comprising a variant of the human vBGF-D disclosure of the invention. In one instance a polypeptide is claimed comprising a least one mutation selected from the group consisting of comparising a lirst monomer derived from VBGF-D having at least the mutation BSTR and optionally comprising a second monomer apply period is claimed comprising a first monomer containing a substitution consisting of SIOR, SIOR and BSTR (although the residue at position 10 is an Ile), and/or in the other VBGF-D derived monomer at least one substitution consisting of T38R, T38E, F39R, F39R, T8ER and DTGE. NOTE: This sequence is not represented in the body of the specification but has been xxx
Novel single-chain dimeric polypeptide for inhibiting angiogenesis, binds to extracellular ligand-binding domain of vascular endothelial growth factor type 2/type 3 receptor but does not activate the receptor.
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lymph vessel endothelial cell; VEGF receptor-3; neoplastic disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM47933 standard; protein; 110 AA.
                                                                                                                         Claim 11; Page; 71pp; English.
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Best Local Similarity 100.
Matches 9; Conservative
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Preparing active growth factor dimers from inclusion bodies in high yield.
                             mouse VEGF-D polypeptide.
                                                                                                                                                                                                                                                                                      WPI; 1999-278785/24.
   WPI; 2002-049310/06
                                                                                                                                      Best Local Similarity
Matches 9; Conserv
                                                                                                                          Sequence 110 AA;
                                                                                                                                                                                                                     pharmaceutical
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                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                   Query Match
                                                                                                                                                                                                         Human
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New endothelial growth factor polypeptide and polynucleotides, useful for diagnosing, preventing, and treating cancer and other conditions or diseases involving angiogenesis and cell proliferation.
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282. .287

Note= "Region not represented in SEQ ID 1 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NVR, human; endothelial growth factor; cytostatic; cancer; angiogenesis; cell proliferation; revascularisation; amputation; vasculogenesis; transplant; brain; breast; intestine; kidney; lung; ovary; pancreas; prostate; uterus; gene therapy.
                        This invention describes the novel preparation of biologically active dimers of recombinant human growth factors of the cysteine knot family starting from cellular inclusion bodies. Such dimers are are useful in pharmaceutical compositions and the method provides yields of 31-39.7%, in examples, compared with about 10% for the conventional method (see Biochemistry, 28 (1989) 2956). AAYO8278-YO8301 are human growth factor protein fragments used in the method of the invention
                                                                                                                                                                                                                                                    Length 178;
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                                                                                                                                                                                                                                                 Score 43; DB 2;
Pred. No. 27;
); Mismatches C
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100.0%; Pr
tive 0;
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Claim 14; Page 9; 14pp; German.
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Best Local Similarity 100.
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                                                                                                                                                                                                                Sequence 178 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG73779;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
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      The invention relates to a method for activating only vascular and other an active amount of a composition comprising a cell bearing the receptor an active amount of a composition comprising a cell bearing the receptor an active amount of a composition comprising a colypeptide having at least 90%, preferably 95%, sequence identity with the mouse vEGF-D polypeptide or its fragment. The polypeptide is useful for activation of specifically activates VEGF receptor-3 which results in proliferation of 1 ymph vessel endothelial cells. The polypeptide is useful for activating only vEGF receptor-3 and is therefore useful for stimulating proliferation and/or maintaining of only lymph vessel endothelial cells. The polypeptide is also useful in the diagnosis of a neoplastic disease characterized by an increase in lymph vessel endothelial cells. The mouse vEGF-D has two isoforms. The longer amino acid sequence designated mVEGF-C vEGF-D has two isoforms. The longer amino acids (AAM47932) after cresidue 30 and diverges in the C-terminal sequence after residue 317 cresidue 30 and diverges in the C-terminal sequence after residue 30 compared to the shorter isoform mVEGF-D2, which diverges after residue 312 comparing residues 92-201 of the full length mouse VEGF-D2 protien of comparing a sequence is that of the full length mouse VEGF-D2 protien of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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                                                                                       Specific activating of VEGF receptor-3, useful for stimulating proliferation and/or maintaining of only lymph vessel endothelial cells, by administration of a polypeptide having high sequence identity with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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100.0%; Pred. No. 16;
ive 0; Mismatches (
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                                                                                                                                                                                                         Claim 1; Page 41; 41pp; English
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This invention describes a novel human endothelial growth factor polypeptide which has cycostatic activity. The polypeptide and its encoding polymucleotide are useful in the diagnosis, prevention, and treatment of cancer and other conditions or diseases involving

Claim 1; Fig 1A-B; 28pp; English.

Weich H, Erdmann H;

Rinas U,

Mueller C,

acceleration of angiogenesis in

(VEGF-D2). VEGF-D2 can be used for

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New isolated vascular endothelial growth factor-D - used to products for use in e.g. modifying angiogenesis or treating or intestinal disorders.
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96AU-00003554.
96US-0031097P.
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                                                                                                                      Conservative
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Best Local Similarity
9, Conserve
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Sequence 287 AA;
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14-NOV-1996
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10-FEB-1997
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AAW53243

ID AAW53243

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AC AAW53

DT 03-AU

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The sequence is that of mouse lung vascular endothelial growth factor D2

Claim 16; Page 64-65; 101pp; English.

develop lung, heart

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                                                                                                         inhibitors of NVR may be used to suppress or prevent angiogenesis and thus prevent the growth and development of cancers such as cancer of the brain, breast, intestine, kidney, lung, ovary, pancreas, prostate or uterus. The products of the invention can be used for gene therapy. This sequence represents the human NVR protein described in the disclosure of
angiogenesis and cell proliferation. NVR may also be used to promote revascularisation following traumatic amputation and surgical reconstruction or added to a tissue culture to promote vasculogenesis in tissues for autologous or heterologous transplant. Antagonists or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vascular endothelial growth factor; VBGF-D; angiogenesis; modification; acceleration; wound healing; tissue; organ; transplants; collateral dirculation; infarction; arterial stenosis; coronary artery disease; inhibition; cancer; treatment; diabetic retinopathy; lung disorders; blood circulation; gaseous exchange; chronic obstructive airway disease; intestinal malabsorptive syndrome; biopsy; metastatic risk; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                          Length 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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100.0%; Pred, No. 44;
iive 0; Mismatches (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosis; congestive heart failure.
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                                                                                                                                      70.5%; Score 43; DB 2; Length 321; 100.0%; Pred. No. 49;
                                                                                                                                                      0; Indels
                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                    Search completed: September 5, 2004, 09:55:11 Job time : 37.1111 secs
                                                                                                                                                     9; Conservative
                                                                                                                                                                                168 ISVPLTSVP 176
                                                                                                                                                                 2 ISVPLTSVP 10
                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                       Sequence 321 AA;
                                                                                                                                                   Matches
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for detection and diagnosis

wound healing, tissue or organ transplantation. Or to establish

collateral circulation in tissue infarction or arterial stenosis, such as

coronary artery disease, and inhibition of angiogenesis in the treatment

of cancer or of diabetic retinopathy. It can also be used in the

treatment of lung disorders to improve blood circulation in the lung

and/or gaseous exchange between the lungs and the blood stream or to

improve blood circulation to the heart and 02 gas permeability in cases

of cardiac insufficiency, to improve blood flow and gaseous exchange in

chronic obstructive airway disease, or to treat malabsorptive syndromes

chronic obstructive airway disease, or to treat malabsorptive syndromes

to the intestinal tract. Quantitation of VBGF-D in cancer blopsy

specimens may be useful as an indicator of future metastatic risk.

Antagonists can be used for treating e.g. conditions such as congestive

cheart failure, involving accumulations of fluid in the lung resulting

from increases in vascular permeability. The products can also be used

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(without alignments)
112.199 Million cell updates/sec
                                                                                                                                                                                 September 5, 2004, 10:00:15 ; Search time 30.8889 Seconds
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(9972_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
(9972_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1298764 seqs, 315065143 residues
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                                                                                                               OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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61
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                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		Seguence /, Appil	Semionce 25, Appl		•	Somience 23, Appl	4	Sequence 11, Appl		Sequence 16, Appr	Sequence I, Appli	Sequence 3, Appli	ζ,	Ċ	٠٥	Sequence 8, Appli
SUMMARIES	ID	US-09-761-636A-7	US-09-761-636A-23	US-09-761-636A-26	US-09-761-636A-24	US-09-761-636A-25	US-09-761-636A-13	US-10-139-876-11	TIS-10-086-623-18	US-10-260-539-18	US-09-761-6364-1	US-09-956-095-3	US-09-219-345b-1	TIS-10-779-731-1	US-09-847-524-6	TC-10-252-152 B	0-551-555-01-60
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ф	Query	100.0	96.7	93.4	88.5	85.2	74.6	70.5	70.5	70.5	70.5	70.5	70.5	70.5	70.5	70.5	,
	Score	61	59	57	54	52	45.5	43	43	43	43	43	43	43	43	43	
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Segment 1	1 4	rσ	ìσ		· ~	٠,	Semience 11 appli	-	Semience A anni-		, v		, r	ה	ī -	1 .	, ,	v -	Semience 13, Appl	٠,	1 -	íα	Sections 0, Appli		ָּבְּרָ בְּבָּרָ	100	, ,	14, Ap	576,	Sequence 576, App
US-10-044-622-1	US-09-847-524-4	US-10-274-953-9	US-10-161-694-9	US-10-274-953-3	US-10-161-694-3	US-09-956-095-2	US-09-219-345A-11	US-09-795-006A-119	US-09-375-248-6	US-09-765-534B-22	US-10-661-740-6	US-10-262-538-26	US-10-274-953-5	US-10-161-694-5	US-10-174-930-1	US-09-852-209A-13	US-09-847-524-2	US-10-439-337A-13	US-10-303-997B-13	US-10-139-876-2	US-10-131-600-13	US-10-274-953-8	US-10-161-694-8	US-10-139-876-4	US-10-195-730-172	US-10-799-747-172		TIG-10-308-14	110 10 100 110 110	US-T0-199-670-576
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43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	42	42	41	40		7
16	17	18	19	20	21	22	23	24	25	26	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	2

## ALIGNMENTS

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US-09-761-636A-7

Sequence 7, Application US/09761636A

Sequence 7, Application US/09761636A

BAPLICANT: ALTEN, Mac

APPLICANT: ALTEN, Application

APPLICANT: HUGHES, Richard

APPLICANT: HUGHES, Richard

APPLICANT: HUGHES, Richard

APPLICANT: HUGHES, Richard

APPLICANT: HUGHES, Richard

APPLICANT: HUGHES, Richard

APPLICANT: HUGHES, Richard

APPLICANT: HUGHES, Richard

APPLICANT: HUGHES, Richard

APPLICANT: HUGHES, Richard

TILE REFERENCE: 1064/48505 Achen et al

CURRENT APPLICATION NUMBER: US/09/761,636A

FRIDE ADATE: 2000-01-18

PRIOR APPLICATION NUMBER: US 60/176,293

PRIOR APPLICATION NUMBER: US 60/204,590

PRIOR APPLICATION NUMBER: US 60/204,590

PRIOR APPLICATION NUMBER: US 60/204,590

PRIOR PILING DATE: 2000-01-16

NUMBER OF SEQ ID NOS: 34

SOFTWARE: Patentin version 3.0

SEQ ID NO 7

LENGTH: 11

CORGANISM: Homo sapiens

US-09-761-636A-7

Ouery Match

Best Local Similarity 100.0%; Pred. No. 0.0036;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps

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1 CISVPLESVPC 11
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Db 1 CISVPLTSVPC 11

0;

US-09-761-636A-23 ; Sequence 23, Application US/09761636A ; Patent No. US20020065218A1

RESULT 2

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APPLICANT: ACHEN, Marc
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT FILING DATE: 2000-101-18
PRIOR PILING DATE: 2000-01-18
PRIOR PLICATION NUMBER: US 60/176,293
PRIOR PLICATION NUMBER: US 60/204,590
PRIOR APPLICATION NUMBER: US 60/204,590
PRIOR PLING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTI VETRION 3.0
SEQ ID NO 25
LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13, Application US/09761636A
Sequence 13, Application US/09761636A
Sequence 13, Application US/09761636A
Sequence 13, Application
GENERAL INFORMATION:
APPLICANT: ACHEN, Marc
APPLICANT: HUGHES, Richard
APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT FILING DATE: 2001-01-18
CURRENT FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/176,293
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 11;
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                                                                                                                                                                                                                                                                                                                                                                  Score 54; DB 9;
Pred. No. 0.046;
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Pred. No. 0.095;
                       FILE REFERENCE: 1064/48505 Achen et al CURRENT APPLICATION NUMBER: US/09/761,636A CURRENT FILING DATE: 2001-01-18 PRIOR PRILING DATE: 2000-01-18 PRIOR FILING DATE: 2000-01-18 PRIOR FILING DATE: 2000-01-18 NUMBER OF SEQ ID NOS: 34 SOFTWARE: Patentin version 3.0 SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-761-636A-25;
Sequence 25, Application US/09761636A;
Patent No. US20020065218A1;
GENERAL INFORMATION:
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72.7%;
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72.7%;
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US-09-761-636A-25
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US-09-761-636A-24
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Best Local Similarity 72...
Best Local Similarity 72...
Conservative
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1 CITIPLTSLPC 11
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Matches 8; Conserv
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US-09-761-636A-13
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Sequence 26, Application US/09761636A

Sequence 26, Application US/09761636A

Sequence 26, Application US/09761636A

GENERAL INFORMATION:

APPLICANT: ACHEN, MACHEN, Richard

APPLICANT: CENDROM, Angela

TILLE OF INVENTION: VEGP-D/VEGF PEPTIDOMIMETIC INHIBITOR

TILLE REFERENCE: 1664/4850 Achen et al

CURRENT APPLICATION NUMBER: US/09/761,636A

CURRENT PILING DATE: 2001-01-18

PRIOR FILING DATE: 2000-01-18

PRIOR FILING DATE: 2000-01-18

PRIOR FILING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PATENTING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 34
                                          APPLICANT: ACHEN, Marc
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: HUGHES, Richard
APPLICANT: HUGHES, Richard
APPLICANT: HUGHES, Richard
APPLICANT: GENDRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT FILING DATE: 2001-01-18
PRIOR PILING DATE: 2000-01-18
PRIOR PILING DATE: 2000-01-18
PRIOR PILING DATE: 2000-01-18
PRIOR PILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.0
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81.8%; Pred. No. 0.015;
tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 59; DB 9; Length 11;
Pred. No. 0.0074;
1; Mismatches 0; Indels
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Sequence 24, Application US/09761636A
Patent No. US20020065218A1
GENERAL INFORMATION:
APPLICANT: ACHEN, Marc
APPLICANT: HUGHES, Richard
APPLICANT: CENDRON, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
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Best Local Similarity
Matches 9; Conserv
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US-09-761-636A-24
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US-09-761-636A-26
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LENGTH: 11
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ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 23
LENGTH: 11
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Gaps

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APPLICANT: UUTELA, Marko
APPLICANT: UUTELA, Marko
APPLICANT: UUTELA, Marko
APPLICANT: ALITALO, Kari
APPLICANT: ALITALO, Kari
APPLICANT: ALITALO, Kari
APPLICANT: HELDIN, Carl-Henrik
TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES TH
FILE REFERENCE: 1064/4483302
CURRENT APPLICATION NUMBER: US/10/086,623
PRIOR PLILING DATE: 2000-03-04
PRIOR APPLICATION NUMBER: US 60/107,852
PRIOR APPLICATION NUMBER: US 60/113,997
PRIOR APPLICATION NUMBER: US 60/13,997
PRIOR FILING DATE: 1999-10-04
PRIOR FILING DATE: 1999-10-04
PRIOR FILING DATE: 1999-10-04
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: US 60/157,756
PRIOR FILING DATE: US 60/157,756
PRIOR FILING DATE: US 60/157,756
PRIOR FILING DATE: US 60/157,756
PRIOR FILING DATE: US 60/157,756
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PRIOR FILING DATE: US 60/157,756
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; OTHER INFORMATION: PDGF/VEGF-homology domain of VEGF-D
US-10-086-623-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 70.5%; Score 43; DB 13; Best Local Similarity 100.0%; Pred. No. 18; Matches 9; Conservative 0; Mismatches 0
                                                                               CURRENT FILING DATE: 2000-03-04

PRIOR APPLICATION NUMBER: US 60/107,852
PRIOR PILING DATE: 1998-11-10

PRIOR PILING DATE: 1998-11-10

PRIOR FILING DATE: 1998-12-28

PRIOR FILING DATE: 1998-12-28

PRIOR FILING DATE: 1999-10-26

PRIOR PELING DATE: 1999-08-26

PRIOR PILING DATE: 1999-08-26

PRIOR PILING DATE: 1999-10-04

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-11-10

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 2000-10-19

NUMBER OF SEQ ID NOS: 42

SOFTWARE: PALENTIN VERSION 3.1

SEQ ID NO 18

FRIORTH: 81
                                                            CURRENT APPLICATION NUMBER: US/10/086,623
CURRENT FILING DATE: 2000-03-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18, Application US/10260539
Publication No. US20030073637A1
GENERAL INFORMATION:
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LI, Xuri
PONTEN, Annica
UUTELA, Marko
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APPLICANT: HELDIN, Carl-Henrik
TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
US-10-139-876-11
i Sequence 11. Application US/10139876
j Publication No. US20020123481A1
j GENERAL INFORMATION:
i APPLICANT: Oliviero, Salvatore
i TITLE OF INVENTION: C-FOS Induced Growth Factor (Figf) And Dna Encoding Same
i TITLE OF INVENTION: C-FOS INDUCED GROWTH Factor (Figf) And Dna Encoding Same
i TITLE OF INVENTION: C-FOS 102-05-07
i CURRENT APPLICATION NUMBER: US/10/139,876
i PRIOR FILING DATE: 1998-03-18
i PRIOR FILING DATE: 1998-03-18
i PRIOR FILING DATE: 1996-09-30
i PRIOR FILING DATE: 1996-09-30
i PRIOR APPLICATION NUMBER: GB9612368.2
i PRIOR APPLICATION NUMBER: GB951928.7
i PRIOR FILING DATE: 1995-09-30
i PRIOR FILING DATE: 1995-09-29
i NUMBER OF SEQ ID NOS: 20
i SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 0.93;
0; Mismatches 0; Indels
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Pred. No. 11;
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PRIOR FILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: US 60/204,590
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.0
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Publication No. US20020164710A1
GENERAL INFORMATION:
APPLICANT: BAIRSSON, Ulf
APPLICANT: AASE, Karin
APPLICANT: LI, Xuri
APPLICANT: UNTELA, Marko
APPLICANT: UNTELA, Marko
APPLICANT: ALITALO, Kari
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Best Local Similarity 100.0%; Pr
Conservative 0;
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90.9%;
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Best Local Similarity 90.9
Marches 10; Conservative
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PONTEN, Annica
UUTELA, Marko
ALITALO, Kari
OESTMAN, Arne
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                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
US-09-761-636A-13
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ORGANISM: Homo sapiens
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US-10-086-623-18
                                                                                                                                                     SEQ ID NO 13
LENGTH: 10
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                                                                                                                                                                         70.5%; Score 43; DB 9; Length 109; 100.0%; Pred. No. 24; tive 0; Mismatches 0; Indels
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 109
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 109
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                      2 ISVPLTSVP 10
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                                                                               TYPE: PRT
ORGANISM: Homo sapiens
US-09-956-095-3
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US-09-219-345A-1
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US-10-779-731-1
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| Sequence 3. Application US/09956095
| Sequence 3. Application US/09956095
| Patent No. US20020102260A1
| Patent No. US20020102260A1
| Patent No. US20020102260A1
| APPLICANT: ACHEN, Marc G.
| APPLICANT: STACKER, Steven A. TITLE OF INVENTION: WETHOUS FOR TREATING NEOPLASTIC DISEASE CHARACTERIZED BY TITLE OF INVENTION: VASCULAR ENDOTHELLAL GROWTH FACTOR D EXPRESSION, FOR SCREENING TITLE OF INVENTION: VASCULARIZATION OF TISSUE
| TITLE OF INVENTION: VASCULARIZATION OF TISSUE
| FILE REFERENCE: 1064/48666PC | CURRENT APPLICATION NUMBER: US/09/956,095 | CURRENT APPLICATION NUMBER: US/09/956,095 | PRIOR PILING DATE: 2001-09-20 | PRIOR APPLICATION NUMBER: 60/234,196 | PRIOR FILING DATE: 2000-09-20 | PRIOR PILING DATE: 2000-09-20 | PRIOR FILING DATE: 2000-09-20 | PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR 
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; Sequence 1, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
    APPLICANT: ACHEN, Marc
; APPLICANT: CENDROW, Angela
    APPLICANT: HUGHES, Richard
    TITLE OF INVENTION: VEGED/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
    TITLE OF INVENTION: UNDER: US/09/761,636A
    CURRENT FILING DATE: 2000-01-18
    PRIOR FILING DATE: 2000-01-18
    PRIOR FILING DATE: 2000-01-18
    PRIOR FILING DATE: 2000-05-16
    NUMBER OF SEQ ID NOS: 34
    SOFTWARE: PATENTIN VEYSION 3.0
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, OTHER INFORMATION: Amino acid residues of Vall01-Pro196 of VEGF-D
US-09-761-636A-1
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Dest Local Similarity 100.0%; Pred. No. 18;

Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                  FEATURE:

"NAME/KEY: misc_feature

"NAME/KEY: misc_feature

"OTHER INFORMATION: PDGF/VEGF-homology domain of VEGF-D
US-10-260-539-18
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Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: Homo sapiens
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                     LENGTH: 81
TYPE: PRT
ORGANISM: Homo Bapiens
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LENGTH: 96
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| Publication No. US20030211101A1
| GENERAL INFORMATION:
| APPLICANT: Wise, Lyn M
| APPLICANT: Wise, Lyn M
| APPLICANT: Stacker, Stephen B
| APPLICANT: Stacker, Stephen B
| APPLICANT: Stacker, Stephen B
| APPLICANT: Stacker, Stephen B
| APPLICANT: Stacker, Stephen B
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| APPLICANT: Stacker, Stephen B
| APPLICANT: Stacker, Stephen B
| APPLICANT: Stacker, Stephen B
| APPLICANT: Stacker, Stephen B
| TITLE OF INVENTION: VIRUS NZ2 BINDS AND ACTIVATES MAMMALIAN VEGF
| FILE REPERBENCE: Sequence Listing for 09/431,833
| CURRENT APPLICATION NUMBER: US/09/431,888A
| FRIOR APPLICANT: NUMBER: EARLIER FILING DATE: 1999-11-02
| PRIOR APPLICANT: NUMBER: EARLIER FILING DATE: 1998-11-03
| NUMBER OF SEQ ID NOS: 11
| SEQ ID NO 8
| LENGTH: 197
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Publication No. US20030166523A1
GENERAL INFORMATION:
APPLICANT: ACHEN, Marc G
APPLICANT: STACKER, Steven A
TITLE OF INVENTION: A METHOD FOR ACTIVATING ONLY THE VASCULAR ENDOTHELIAL
TITLE OF INVENTION: A METHOD FOR ACTIVATING ONLY THE VASCULAR ENDOTHELIAL
TITLE OF INVENTION: A COURT HACTOR RECEPTOR-3 AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/847,524
CURRENT PILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
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                                                                             70.5%; Score 43; DB 16; Length 109; 100.0%; Pred. No. 24; Cive 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 9; Conservative
                                                                     Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) TYPE: PRT
) ORGANISM: Murinae gen. sp.
US-09-847-524-6
; ORGANISM; Homo sapiens
US-10-779-731-1
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-10-352-153-8
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Gaps
    .,
  Indels
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 0; Mismatches
                                                                                               Search completed: September 5, 2004, 10:29:18 Job time : 30.8889 secs
9; Conservative
                                                     92 İSVPLTSVP 100
                         2 ISVPLTSVP 10
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

5, 2004, 09:55:30 ; Search time 9.77778 Seconds September Run on:

(without alignments)
58.079 Million cell updates/sec

US-09-761-636A-7 Title: Perfect score:

1 CISVPLTSVPC 11

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

389414 seqs, 51625971 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

lssued_Patents_AA:*
l: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
l: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
l: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
l: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
l: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
l: /cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
lcgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description		ì	i o		Sequence 3, Appin	ח ו	Semience 3, Appii	0 4		equence		Seguence z, Appii		Seguence 34, Appl	Somiones 1/910, A	Sequence 6, Appli	Sequence 5, Appli	Fatent No. 5220013	sednence 23997, A	Sequence 29818, A	Sequence 227, App	22	22	2		, ,	7 -	Sequence 1, Appli	
	ID	US-09-469-186-1	-09-46	43	US-08-915-795-9	-08-91	-08-91	US-08-915-795-8	-09-134	US-08-959-004-5	US-09-328-352-7636	US-10-042-810-2	US-10-042-810-4	US-08-861-774E-94	US-09-252-991A-17910	US-09-508-7708-6	T KAFC-005-00-011	-3/0A-	IIS-09-252-9918-22907	TIG- 00 C3C 00 C3C	115 00 C21 00 C1	US-US-635-886C-227	US-U8-9/4-69UC-22/	US-08-134-231C-22	US-08-728-160-22	US-08-612-973-32	US-08-927-597-32	US-08-923-856-1	US-09-216-294-1	
	DB	4	4	4	m	m	٣	e	4							4		H 40										2		
	Query Match Length	109	109	197	321	325	354	358	79	663	009	1248	1278	388	409	533	534	106	147	150	1 1	103	1 0	107	207	208	208	299	299	
de	Query	70.	70.5	0	70.5	70.5	70.5	70.5	9.59	62.3	60.7	60.7	60.7	59.0	59.0	59.0	59.0	57.4	57.4	57 4	57.4	57.4			57.4	57.4	57.4	57.4	57.4	
	Score	43	43	43	43	43	43	43	40	38	37	37	37	36	36	36	36	35	35	35	7	) (C	) C	י נ	45	35	32	35	35	
	Result No.	7	(7)	e	4	2	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	1 0	67	47	25	26	27	

Sequence 202, App Sequence 226, App Sequence 202, App	226, 20, 20,			Sequence 58, Appl Sequence 58, Appl Sequence 58, Appl Sequence 58, Appl Sequence 58, Appl
ব ব ব	3.19 4 US-08-974-690C-226 3.63 1 US-08-484-105-20 3.63 1 US-08-484-106-20 3.42 4 IIS-09-561-7005-12	4-1-	38 1 US-08-189-331-111 38 2 US-08-471-939-111 38 2 US-08-471-800-111 38 2 US-08-471-800-111	72 3 US-08-722-719-58 72 4 US-09-334-951-58 72 4 US-09-334-923A-58 72 4 US-09-334-954A-58
28 35 57.4 3 30 35 57.4 3 31 35 57.4 3	-	34 55.7 34 55.7 34 55.7	38 34 55.7 39 34 55.7 40 34 55.7 41 34 55.7	

## ALIGNMENTS

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Gaps
                                                  FALCHIA NO. 920-940-4

APPLICANT: ACHEN, MARC G.
APPLICANT: STACKER, SECVE A.
APPLICANT: STACKER, SECVE A.
TITLE OF INVENTION: ANTIDDIES TO TRUNCATED VEGF-D AND USES THEREOF FILE REFERENCE: ACHEN et al.-1064-44660
CURRENT APPLICATION NUMBER: 105/09/469,186
CURRENT FILING DATE: 1999-12-21
EARLIER FILING DATE: 1999-12-21
EARLIER PILING DATE: 1999-05-17
NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
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                  Sequence 1, Application US/09469186
Patent No. 6383484
                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-469-186-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 9; Conserv
JS-09-469-186-1
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2 ISVPLTSVP 10 76 ISVPLTSVP 84 à g

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RESULT 2

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ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C. STREET: 1200 G Street, NW, Suite 700 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,795
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: EVANA; Joseph D. 5,269
REGISTRATION NUMBER: 1064/42983
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAK: (202) 628-8800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08915795; Patent No. 6235713
GENERAL INFORMATION:
APPLICANT: Marc G. ACHEN
APPLICANT: Steven A. STACKER
APPLICANT: Steven A. STACKER
APPLICANT: Steven A. STACKER
APPLICANT: Steven A. STACKER
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTY: United States of America ZIP: 20005
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: N/A
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                    LENGTH: 321 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein SOURCE: TYPE: Mouse Lung US-08-915-795-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 isveirsve 176
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                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Wash STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
US-08-915-795-3
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                                                                                                                                                                                                                                                                                                                                                  yesquence 8, Application US/0943188BA

| Sequence 8, Application US/0943188BA
| Pateant No. 6541008
| GENERAL INFORMATION:
| APPLICANT: Wise, Lyn M
| APPLICANT: Wise, Lyn M
| APPLICANT: Savory, Lorean J
| APPLICANT: Stephen B
| APPLICANT: Stephen B
| APPLICANT: Stephen B
| APPLICANT: Stephen B
| TITLE OF INVENTION: VIRUS NZ2 BINDS AND ACTIVATES MAWALIAN VEGF
| TITLE OF INVENTION: VIRUS NZ2 BINDS AND ACTIVATES MAWALIAN VEGF
| TITLE OF INVENTION: VIRUS NZ2 BINDS AND ACTIVATES MAWALIAN VEGF
| TITLE OF INVENTION: UNBER: US/09/431,833
| Patent No. 6541008
| CURRENT APPLICATION NUMBER: US/09/431,888A
| CURRENT APPLICATION NUMBER: US/09/431,888A
| CURRENT PILING DATE: 1999-11-02
| EARLIER PILING DATE: 1998-11-03
| WUMBER OF SEQ ID NOS: 11
| SOFFWARE: Patentin Ver. 2.0
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Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

70.5%; Score 43; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                     70.5%; Score 43; DB 4; Length 109; 100.0%; Pred. No. 5.8; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/08915795; Sequence 9, Application US/08915795; Patent No. 6235713; GENERAL INFORMATION:
APPLICANT: Marc G. ACHEN
APPLICANT: Steven A. STACKER
APPLICANT: Steven A. STACKER
APPLICANT: Kari ALITALO
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSES: Evenson, McKeown, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 United States of America
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
                                                                                                               Query Match
Best Local Similarity 100.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 ISVPLTSVP 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , ORGANISM: Homo sapiens
US-09-431-888-8
                   TYPE: PRT
CORGANISM: Homo sapiens
US-09-469-185-1
                                                                                                                                                                                                          2 ISVPLTSVP 10
                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 8
LENGTH: 197
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US-08-915-795-9
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                                                                                                                                                                                                                                                                                                                          RESULT 3
US-09-431-888-8
LENGTH: 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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DB 3; Length 321;
18;
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           SOFTWARE; Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 70.5%; Score 43; DB Best Local Similarity 100.0%; Pred. No. 18; Matches 9; Conservative 0; Mismatches
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                   APPLICALL.

FILING DATE:
    CLASIFICATION: 536
ATTORNEY/AGENT INFORMATION:
    NAME: EVANS, JOSEPH D.
    REGISTRATION NUMBER: 26,269
    REFERENCE/DOCKET NUMBER: 1064
    TELECOMUNICATION INFORMATION:
    TELEPHONE: (202) 628-8800
    TELEPHONE: (202) 628-8800
                                                                                                                                                                                                                                                                                                 TELEX: N/A
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 9; Conserv
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Best Local 8
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                                                                                                                                                                    Ouery Match 70.5%; Score 43; DB 3; Length 325; Best Local Similarity 100.0%; Pred. No. 18; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
F: 1200 G Street, NW, Suite 700
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 70.5%; Score 43; DB 3; Length 354; Best Local Similarity 100.0%; Pred. No. 20; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY. United States of America
ZIP: 20005
ZIP: 20005
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,795
FLING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
                                                                                                                                                                                                                                                                                                                                                             RESULT 6
US-08-915-795-5
Sequence 5, Application US/08915795
Patent No. 6235713
GENERAL INFORMATION:
APPLICANT: Marc G. ACHEN
APPLICANT: Active F. WILKS
APPLICANT: Steven A. STACKER
APPLICANT: Steven A. STACKER
APPLICANT: Steven A. STACKER
APPLICANT: Rai ALITALO
TILLE OF INVENTION:
MUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
                                        MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: Human Breast
US-08-915-795-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: N/A
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 354 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: NO ORIGINAL SOURCE: TISSUE TYPE: Human Lung
        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, N
                                                                                                                                                                                                                                                                                            139 ISVPLTSVP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                           2 ISVPLTSVP 10
                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-915-795-5
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Sequence 4906, Application US/09134000C
| Sequence 4906, Application US/09134000C
| Patent No. 6617156
| GENERAL INVERMATION:
| APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION:
| TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
| CURRENT APPLICATION NUMBER: US/09/134,000C
| CURRENT FILING DATE: 1999-08-13 | PRIOR APPLICATION NUMBER: US 60/055,778 |
| PRIOR FILING DATE: 1997-08-15 | NUMBER OF SEQ ID NOS: 6812 |
| SOFTWARE: PatentIn version 3.1 | SENGTH: 79 |
| TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                      ALUKESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C. STREET: 1200 G Street, NW, Suite 700 CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.5%; Score 43; DB 3; Length 358; 100.0%; Pred. No. 20; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,795
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/42983
TELECOMMUNICATION INFORMATION:
US-08-915-795-8

Sequence 8, Application US/08915795

Patent No. 6235713

GENERAL INFORMATION:
APPLICANT: Marc G. ACHEN
APPLICANT: Steven A. STACKER
APPLICANT: Steven A. STACKER
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
ADDRESSEE: Evenson, McKeown, Edwar
                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: United States of America ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELBERX: (202.
TELEFAX: (202.
TELEF X: N/A
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
""DE: amino acids
""PE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (202) classes and (202) classes (202) 628-8844
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Sequence 2, Application US/10042810

Patent No. 6570003

GENERAL INFORMATION:
APPLICANT: Hu, Yi
APPLICANT: Burnett, Michael
APPLICANT: Burnett, Michael
TITLE OF INVENTION: No. 6570003el Human 7TM Proteins and Polynucleotides Encoding th
TITLE OF INVENTION NUMBER: US/10/042,810
CURRENT PILING DATE: 2002-01-09
CURRENT PILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 5
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence No. 657003
Sequence No. 657003
GENERAL INFORMATION:
APPLICANT: Burnett, Michael
APPLICANT: Burnett, Michael
APPLICANT: Zambrowicz, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: LEX-029-USA
CURRENT APPLICATION NUMBER: US/10/042,810
                                                                             RESULT 10

US-09-328-352-7636

US-09-328-352-7636

Sequence 7636, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:

APPLICANT: GATY L. Breton et al.

TITLE OF INVENTION: NUCLECT ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION UNDHERR: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 7636
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 4; I
Pred. No. 3.1e+02;
3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                               60.7%;
60.0%;
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Matches 6; Conservative
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Matches 6, Conservative
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479 CISVPLTFI 487
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ORGANISM: homo sapiens
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US-10-042-810-2
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                                                                     . IOCATION: (10)...(15). COTHER INFORMATION: Amino acids 10 & 15 are Xaa wherein Xaa = any amino acid. US-09-134-000C-4906
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Sequence 5, Application US/08959004

Patent No. 6197543

GENERAL INPORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Corley, Neil C.

APPLICANT: Corley, Neil C.

APPLICANT: Shah, Purvet

APPLICANT: And Preeti

APPLICANT: And Purvet

TITLE OF INVENTION: HUMAN VESICLE MEMBRANE PROTEIN-LIKE

TITLE OF INVENTION: PROTEINS

TITLE OF INVENTION: PROTEINS

WUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38; DB 3; Length 663;
Pred. No. 2.4e+02;
1; Mismatches 1; Indels
                                                                                                                                                 4; Length 79;
                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIDIE
OPERATING SYSTEM: DOS
SOFTWARE: FASLSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/959,004
                                                                                                                                                 Score 40; DB 4
Pred. No. 12;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: Herewith CLASSIFICATION: 514
RICASSIFICATION: 514
RICASSIFICATION DATA:
APPLICATION WINBER:
ATTORNEY, AGENT INFORMATION:
NAME: Billings, Lucy J.
REFERENCY/COCKET NUMBER: 36,749
REFERENCY/COCKET NUMBER: 96,749
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
          ORGANISM: Enterococcus faecalis
FEATURE:
NAME/KEY: MISC_FEATURE
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77.8%;
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                                                                                                                                                   Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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LIBRARY: ADRETUT06
CLONE: 2822412
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66 CITVPLTAKP 75
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STRANDEDNESS:
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US-09-252-991A-17910
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APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MACC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEAR SERIES AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
ERIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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Patent No. 6297007

GENERAL INFORMATION:
APPLICANT: Waters, Barbara
APPLICANT: Miao, Vivian
APPLICANT: Miao, Vivian
APPLICANT: Hoo, Yap
APPLICANT: Hoo, Yap
APPLICANT: Hoo, Soow
ITTLE OF INVENTION: METHOD FOR ISOLATION OF BIOSYNTHESIS GENES FOR
ITTLE OF INVENTION: BIOACTIVE MOLECULES
ITTLE OF INVENTION: BIOACTIVE MOLECULES
CURRENT APPLICATION NUMBER: US/08/861,774E
CURRENT APPLICATION NUMBER: US/08/861,774E
NUMBER OF SEQ ID NOS: 94

SOFTWARE: Patentin Ver. 2.0

IENCENTIAL OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF
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US-08-861-774E-94
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Pred. No. 6.8e+02;
1; Mismatches 3; Indels
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Soure 36; DB 3; Length 388; Best Local Similarity 77.8%; Pred. No. 2.8e+02; Matches 7; Conservative 1; Mismatches 1; Indels
CURRENT FILING DATE: 2002-01-09
PRIOR APPLICATION NUMBER: US 60/261,624
PRIOR FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 1278
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Patent No. 6551795
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                 60.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial Sequence
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: homo sapiens
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US-08-861-774E-94
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       Score 36; DB 4; Length 409;
Pred. No. 3e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 533;
                                                                                                                                                                                                                                                                         Class I-type Lysyl-tRNA Synthetase
                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: 1ysyl t-RNA synthetase
; OTHER INFORMATION: construct expressed in Example
US-09-508-370A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.0%; Score 36; DB 4; I 50.0%; Pred. No. 3.9e+02; tive 3; Mismatches 2
                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
AITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/508,370A
CURRENT FILING DATE: 2000-03-10
PRIOR FILING DATE: 1998-09-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: MS DOS
LENGTH: 533
                                                                                                                                                                                                                                                                                                                                              PCT/US98/18968
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                                                                                                                                                  RESULT 15
US-09-508-370A-6
; Sequence 6, Application US/09508370A; Patent No. 6492131
; PATENT No. 6492131
; APPLICANT: Dieter Soll
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Methanococcus maripaludis FEATURE:
     59.0%;
Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 50.07
                                                                                    :| | | | | | 42 USAPCTVVPC 51
                                                                    2 ISVPLTSVPC 11
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84 IGMPLSEIPC 93
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GenCore version 5.1.6
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OM protein - protein search, using sw model

5, 2004, 09:47:29; Search time 13.0505 Seconds September Run on:

(without alignments) 125.302 Million cell updates/sec

US-09-761-636A-8

100 1 CASELGKSTNTFCKPPC 17 Perfect score: Sequence:

Scoring table:

283366 seqs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### methylphosphotries hypothetical prote hypothetical prote epidermal growth f hypothetical prote ribonuclease-relat lytB protein (impochitinase (EC 3.2, acetate kinase homacetate kinase homacetate kinase hom DNA polymerase III protein bli-4D [im protein kinase C ( protein kinase C ( probable membrane lustrin A - Califo ultra-high-sulfur ultra-high-sulfur hypothetical prote testican - human protein T27B7.2 [i probable kexin (BC probable electron vascular endotheli UL77 protein - hum factor H - bovine probable membrane Description SUMMARIES XUBSMM T25169 B96614 A45558 D71882 A39035 B45511 AC1574 AH1220 B38346 A38346 **I30748** S33293 F88968 C69336 QQBEB5 S65551 T05555 S77690 E97808 T08852 A84947 D87803 835362 Query Match Length DB Result No.

hypothetical prote hypothetical prote

hypotherical	methylated Drocc	methylated DNA - [pr	hynothetical prote	hymothetical proto	ada remilatori proc	Glu-renagla amidot	tenidación enney-T.	Table recombination	Transparted	Chipprocept of Hair	Suppressor or nair	DNA-binding protei	Outer membrane pro-	F1 Gardile pic	hypothetical prote
H70717	XYEBOT	AG0789	T17722	696556	G82390	G81325	A43567	A41585	A47214	A42770	F84589	T33741	\$20387	T14703	T15720
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40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1  SESULT 1  SECOND 1  Note 1
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Gaps

0

Length 330; Indels

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hypothetical protein T1SM6.10 [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress) C; Species: Arabidopsis thaliana (mouse-ear cress) C; Species: Arabidopsis thaliana (mouse-ear cress) C; Species: O2-Mar-2001 #sequence_revision 02-Mar-2001 #sequen
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A;Residues: 1-330 <WIL>
A;Residues: 1-330 <WIL>
A;Residues: 1-330 <WIL>
A;Cross-references: EMBL:Z81129; PIDN:CAB03405.1; GSPDB:GN00023; CESP:T23F1.6
A;Experimental source: clone T23F1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 48; DB 2;
Pred. No. 6.6;
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Matches 7; Conserv
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A, Molecule type: DNA
A, Residues: 1-371 <STO>
                                                                                                                                                                                                                         A,Gene: CESP:T23F1.6
A,Map position: 5
A,Introns: 16/3
C,Superfamily: gliadin
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A,Gene: T15M6.10
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methylphosphotriester-DNA alkyltransferase (EC 2.1.1.-) / adaAB operon transcription act Cispecies: Bacillus subtilis
Cispecies: Bacillus subtilis
Cispecies: Judan-1993 #sequence_revision 31-Mar-1993 #text_change 16-Jun-2000
Cinccession: S11483; F65582
R;Morohoshi, F.; Hayashi, K.; Munakata, N.
Nucleic Acids Res. 18, 5473-5480, 1990
Nucleic Acids Res. 18, 5473-5480, 1990
A;Accession: S11483
A;Accession: S11483
A;Molecule type: DNA
A;Reference number: S11483; MUID:91016831; PMID:2120677
A;Accession: S11483
A;Molecule type: DNA
A;Residues: 1-211 < AND
A;Accession: S11483
A;Molecule type: DNA
A;Residues: 1-211 < AND
A;Accession: S11483
A;Molecule type: DNA
A;Residues: Disperimentary N: Mosser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
R;Kunst, F.; Ogasawara, N: Mosser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Bron, S: Brouillet, S.; Bruschi, C.Y.; Caldwell, B.; Capuano, V.; Febrer, C.; Ferrari, E.
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galler
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galler
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Puma, S.; Hosono, S.; Hullo, M.F.
Isch, J.; Harwood, C.R.; Henaut, A.; Holsappel, S.; Hosono, S.; Hullo, A.; Liu, H.; Mausell
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Porteteller
Y; M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Porteteller
Y; Minters, Pobhikawa, H.F.; Zumatenin, B.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Yata, K.; Yoshikawa, A; Athors: Yoshikawa, H.F.; Zumatenin, B.; Yoshikawa, H.; Danchin, A.; Tosato, N.; Araber, A; Athors: Yoshikawa, H.F.; Zumatenin, B.; Yoshikawa, H.; Danchin, A; A; Araber, A; Yaterenne eqtheore of the Gram-positive bacterium Bacillus subtilis
A; Accession: F69580
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A;Cross-references: GB:Z99104; GB:Z99105; GB:AL009126; NID:g2632457; PIDN:CAB11974.1;
A;Experimental source: strain 168
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                      F;103-419/Product: vascular endothelial growth factor C #status experimental <MAT>
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T25169
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Pred. No. 4.5;
0; Mismatches 3; Indels
                                                                                                      Score 58; DB 2; Length 419;
Pred. No. 0.23;
1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.0%;
                                                                                                                   Query Match
Best Local Similarity 71.4%;
Matches 10; Conservative
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143 EFGVATNTFFKPPC 156
                                                                                                                                                                                                                                                                                           4 ELGKSTNTFCKPPC 17
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A;Residues: 1-211 <K
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pyldermal growth factor receptor homolog precursor - fluke (Schistosoma mansoni)
N;Contains: protein-tyrosine kinase (BC 2.7.1.112)
C;Species: Schistosoma mansoni
C;Species: Schistosoma mansoni
C;Species: Schistosoma mansoni
C;Accession: A4558; S27836
R;Shoemaker, C.B.; Ramachandran, H.; Landa, A.; dos Reis, M.G.; Stein, L.D.
A;Title: Alternative splicing of the Schistosoma mansoni gene encoding a homologue of A;Title: Alternative splicing of the Schistosoma mansoni gene encoding a homologue of A;Title: Alternative splicing of the Schistosoma mansoni gene encoding a homologue of A;Title: Alternative splicing of the Schistosoma mansoni gene encoding a homologue of A;Title: Alternative splicing of the Schistosoma mansoni gene encoding a homologue of A;Title: Alternative splicing of the Schistosoma mansoni gene encoding a homologue of A;Title: Alternative splicing of the Schistosoma mansoni gene encoding a homologue of A;Residues: 1-1717 < SHO>
A;Residues: 1-1717 < SHO>
A;Residues: 1-1717 < SHO>
A;Coss-references: EMBL:M86396; NID:g160957; PIDN:AAA29866.1; PID:g160958
A;Note: sequence extracted from NCBI backbone (NCBIP:111129)
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C, Superfamily: Arabidopsis thaliana hypothetical protein F24M12.210
                                                                                                       Query Match
Best Local Similarity 50.0%; Pred. No. 21;
Matches 8; Conservative 2; Mismatches 6; Indels
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Cispecies: Hallotis rufescens (California red abalone)
Cispecies: Hallotis rufescens (California red abalone)
Cispecies: Hallotis rufescens (California red abalone)
Cispecies: Hallotis rufescens (California red abalone)
Cispecies: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
Cispecies: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
Cispecies: 272, 32472-32481, 1997
A;Title: Molecular cloning and characterization of lustrin A, a matrix protein from shell A;Reference number: 216496; MUID:98070424; PMID:9405458
A;Reture: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1428 «SHE>
A;Cross-references: EMBL-AF023459; NID:92723361; PIDN:AAB95154.1; PID:92723362
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A;Residues: 1-1428 «SHE>
A;Cross-references: EMBL-AF021459; NID:92723361; Molecule type: mrNA
A;Residues: 1-1428 «SHE>
A;Cross-references: EMBL-AF021459; NID:92723361; Molecule type: mrNA
A;Residues: 1-1428 «SHE>
A;Cross-references: EMBL-AF021459; NID:92723361; Molecule type: mrNA
A;Residues: 1-1428 «SHE>
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A;Cross-references: EMBL-AF021459; NID:92723361; Molecule type: mrNA
A;Residues: 1-1428 «SHE>
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A;Residues: 1-1428 «SHE>
A;Res
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A;Residues: 1-693 <POH>
A;Cross-references: EMBL:Z73244; NID:g1360427; PID:e245792; PID:g1360428; GSPDB:GN00012;
A;Experimental source: strain S288C
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C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 24-Sep-1999
C;Accession: A38660; B38346
R;Wood, L.; Mills, M.; Hatzenbuhler, N.; Vogeli, G.
J. Biol. Chem. 266, 4024, 1991
A;Tille: Serine-rich ultra high sulfur protein gene expression in murine hair and skin di
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                                                                                                                                                                              Cispecies: Saccharomydes cerevisiae
Cibate: 01-Aug-1995 #sequence_revision 24-May-1996 #text_change 19-Apr-2002
Ciaccession: S64904
R;Pohl, T.M.
submitted to the Protein Sequence Database, May 1996
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                                                                                                      probable membrane protein YLR072w - yeast (Saccharomyces cerevisiae)
N/Alternate names: hypothetical protein L2321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 43.0%; Score 43; DB 2; Length 693; Best Local Similarity 50.0%; Pred. No. 75; Matches 7; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: SGD:S0004062
A;Map position: 12R
C;Keywords: transmembrane protein
F;634-650/Domain: transmembrane #status predicted <TMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        358 SSSLGSSTTYYCRP 371
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                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: S64899
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A; Residues: 1-223 < WO2>
                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S64904
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C,Genetics:
A,Gene: MIPS:YLR072w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pypothetical protein jhp0825 - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Varienty: strain J99
C;Species: Helicobacter pylori
A;Varienty: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 29-Sep-1999
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 29-Sep-1999
C;Accession: D71882
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: D71882
A;Accession: D71882
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-100 cARN
A;Residues: 1-100 cARN
A;Residues: 1-100 cARN
A;Reperimental source: strain J99
C;Genetics:
A;Gene: jhp0825
C;Superfamily: conserved hypothetical protein H10711
A,Gene: SER (Stuberfamily: fluke epidermal growth factor receptor homolog 1; protein kinase homology C,Suberfamily: fluke epidermal growth factor receptor homolog 1; protein kinase homology C,Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; phosphoprotein F;1-19/Domain: signal sequence #status predicted <SIG>F;20-1717/Product: epidermal growth factor receptor homolog 1 #status predicted <MAT>F;20-18-1323/Domain: protein kinase homology <KIN>F;1026-1034/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ribonuclease-related anti-tumor protein - northern leopard frog (fragment)
C;Species: Rana pipiens (northern leopard frog)
C;Date: 31-Uul-1991 #sequence_revision 31-Uul-1991 #text_change 30-Jun-1993
C;Accession: A39035
R;Ardelt, W.; Mikulski, S.M.; Shogen, K.
Biol. Chem. 266, 245-251, 1991
A;Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and earl A;Reference number: A39035; MUID:91093131; PMID:1985896
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Pred. No. 14;
1; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                    Score 44; DB 1; I
Pred. No. 1.2e+02;
2; Mismatches 3;
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61.5%; Pred. No. 14;
tive 1; Mismatches
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                                                                                                                                                                                                                                                                                                                    44.0%;
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Best Local Similarity 58.3%;
Matches 7; Conservative
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1311 ELMRTFNTFCKTP 1323
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Best Local Similarity 61.59
....hes 8; Conservative
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A;Molecule type: protein
A;Residues: 1-104 <ARD>
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Best Local Similarity
Matches 8; Conserv
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Affacession: B45511
R;Samac, D.A.; Hironaka, C.M.; Yallaly, P.E.; Shah, D.M.
Plant Physiol. 93, 907-914, 1990
A;Title: Isolation and characterization of the genes encoding basic and acidic chitinase A;Reference number: A45511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Cross-references: GB:M38240; NID:g166665; PIDN:AAA32769.1; PID:g166666
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;34-76/Domain: hevein chitin-binding domain homology <HCB>
F;89-327/Domain: plant chitinase homology <PCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Listeria innocus
C;Species: Listeria innocus
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: Aci574
C;Accession: Aci574
C;Accession: Aci574
C;Accession: Aci574
C;Accession: C; Buchaud, E; Buchaud, A; Baquero, F; Berche, P; Bloecker
C; Dominguez-Bernal, G; Duchaud, E; Durand, L; Dussurget, O; Entian, K.D.; Fsihi, H
D; Jones, L.M.; Karst, U
Science 294, 849-852, 2001
A;Authors: Kreft, J; Kuhn, M; Kunst, F; Kurapkat, G; Madueno, E; Maitournam, A; Mc
A;Authors: Kreft, J; Simoes, N; Tierrez, A; Vazquez-Boland, J.A.; Voss, H; Wehland
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Wolecule type: DNA
A;Residutes: 1-37 <GLR-AS
A;Crosa-references: GB:AL592022; PIDN:CAC96363.1; PID:g16413591; GSPDB:GN00178
A;Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - Listeria innocua (strain Clip11262)
                                                                                                                                                                                   chitinase (EC 3.2.1.14) precursor, basic - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 22-Jun-1999
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0; Mismatches
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Pred. No.
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larity 72.7%;
Conservative
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Best Local Similarity 50.0%;
Matches 9; Conservative
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C,Superfamily: acetate kinase
                                                         AELGKETGTFTK 243
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     3 SELGKSTNTFCK 14
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es 8; Conserv
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A;Molecule type: DNA
A;Residues: 1-335 <SAM>
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Ciracession: A88346
Ciracesion: A88346
R;Wood, L.; Mills, M.; Hatzenbuhler, N.; Vogeli, G.
J. Biol. Chem. 265, 21375-21380, 1990
A;Title: Serine-rich ultra high sulfur protein gene expression in murine hair and skin A;Reference number: A38346; MUID:91065960; PMID:2250030
A;Status: preliminary
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A;Accession: A84947
                                                                                                                                                                                                                                  A; Residues: 1-21, 'GGCGSGCGGCGSNCGGCGSSCCKPVCC', 22-40, 'GSS', 44-45, 'G', 47-48, 'S', 50, 'GSS'
A,Cross-references: GB:M37760, NID:g200963; PIDN:AAA40107.1; PID:g200964
A,Note: this is a correction
R,Wood, L.; Mills, M.; Hatzenbuhler, N.; Vogeli, G.
J. Biol. Chem. 265, 21375-21380, 1990
A,Title: Serine-rich ultra high sulfur protein gene expression in murine hair and skin A,Reference number: A38346; MUID:91065960; PMID:2250030
A,Accession: B38346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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C;Species: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ultra-high-sulfur keratin 1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M37759; NID:g200961; PIDN:AAA40106.1; PID:g200962 A;Note: the sequence reported in this paper has been corrected. See A38660 C;Superfamily: ultra-high-sulfur keratin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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*Residues: 1-230 <WCo.>
A,Cross-references: GB:M37759; NID:g200961; PIDN:AAA40106.1; PID:g200962
C;Superfamily: ultra-high-sulfur keratin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: A84947 R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H. Nature 407, 81-86, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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41.0%; Score 41; DB 2; Length 223;
Best Local Similarity 41.2%; Pred. No. 57;
Matches 7; Conservative 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 319
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59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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nilarity 41.2%; Pred. No.
Conservative 2; Mismatcl
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A;Molecule type: DNA
A;Residues: 1-319 <STO>
A;Cross-references: GB:AP000398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.7
Matches 8; Conservative
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Best Local Similarity
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R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.

J. Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma

A;Authors: Kreft, J.; Simoes, N.; Tierrez, A.; Varquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Recession: AH1220

A;Recession: AH1220

A;Recession: AH1220

A;Residues: L.37 **CALSA**

A;Residues: Brance: Strain EGD-e

C;Genetics:

A;Genetics:

A;Gen
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Search completed: September 5, 2004, 10:01:18 Job time : 14.0505 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

September 5, 2004, 09:38:39; Search time 7.72727 Seconds (without alignments) 114.554 Million cell updates/sec Run on:

US-09-761-636A-8 100 1 CASELGKSTNTFCKPPC 17 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	pti	O43915 homo sanien	5251 rattm	_	STIM.	homod		homo sani		mus m	rana	arabi			arabidops		_		_			P51559 caenorhabdi		~		P70682 cavia porce	œ	P06215 phaseolus v	P26189 salmonella	Q9pn98 campylobact	œ	O06330 homo sanien	0	4
SUMMARIES	ID	VEGD HUMAN	VEGD_RAT	VEGD_MOUSE	VEGC_MOUSE	VEGC HUMAN	ADAA BACSU	YD83 HUMAN			RN30 RANPI				CHIT ARATH		ACK2_LISMO	TIC1_HUMAN	GLMN MOUSE	UL77 HCMVA	CFAH_BOVIN	BLI4_CAEEL	PCK1_SCHPO	KPC1_COCHE	YOH5_YEAST	PGH2_CAVPO	LPRP_MYCTU	CHIT_PHAVU				SUH HUMAN	SUH_XENLA	SUHL_MOUSE
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35 35 35	37 38	39 40	4, 4, L S	4.4 4.4	45

# ALIGNMENTS

4 X 16 AA REPEATS OF C-X(10)-C-X-C-X(1,3)-C.

(APPROXIMATE) .

OR 99 (IN A MINOR FORM). VASCULAR ENDOTHELIAL GROWTH FACTOR

88 205 354 318

22 89 206 222

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MIM; 300091; -. Gextracellular space; TAS. GO; GO:0005615; C:extracellular space; TAS. GO; GO:0005161; F:platelet-derived growth factor receptor bin. . .; TAS. GO; GO:0005161; F:receptor binding; TAS. GO; GO:0008284; P:positive regulation of cell proliferation; TAS. InterPro; IPR0004153; CXXCX_repeat.

InterPro; IPR000072; PD_growth_factor.

Pfam; PF03128; CXXXC; 3.

ProDom; PP0341; PDGF; 1.

ProDom; PD001629; PD growth_factor; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; SMO0141; PDGF; 1. PROSITE; PS00249; PDGF; 1. PROSITE; PS00249; PDGF 1; 1. PROSITE; PS50278; PDGF 2; 1. Anglogenesis; Mitogen; Growth factor; Glycoprotein; Signal; Repeat; Cleavage on pair of basic residues; Multigene family. SIGNAL 1. 21 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, Y12864, CAA73371.1; --
EMBL, Y12865, CAA73371.1; --
EMBL, Y12865, CAA73371.1; JOINED.
EMBL, Y12865, CAA73371.1; JOINED.
EMBL, Y12869, CAA73371.1; JOINED.
EMBL, Y12869, CAA73371.1; JOINED.
EMBL, Y12870, CAA73371.1; JOINED.
EMBL, AJO00185; CAA03942.1; --
EMBL, BCOZY948, AAHZ7948.1; --
HSSP, PLS692; 1VPP.
Genew, HGNC:3708; FIGF.
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121 ASELGKSTNTFFKPPC 136
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Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                DISULFID
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VEGD_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteolytic processing which generates grown factor. Introducing a proteolytic processing which generates non-covalent homodimers...;

U. Biol. Chem. 274:32127-32136(1999).

U. Biol. Chem. 274:32127-32136(1999).

I. Biol. Chem. 274:32127-32136(1999).

I. Biol. Chem. 274:32127-32136(1999).

I. Biol. Chem. 274:32127-32136(1999).

I. Biol. Chem. 274:32127-32136(1999).

I. Biol. Chem. 274:32127-32136(1999).

I. Subcation and also has effects on the permeability of blood midration and also has effects on the permeability of blood midration and also in the factor as vessels. May function in the formation of the venous and lymphatic vascular systems during embryogenesis, and also in the maintenance of differentiated lymphatic endothelium in adults. Binds and activates WEGFR-2 (FHK.) and VEGFR-3 (FH.4) receptors.

I. SUBCELLULAR LOCATION: Secreted.

I. SUBCELLULAR LOCATION: Secreted.

I. SUBCELLULAR LOCATION: Secreted.

I. TISSUE SPECIFICITY: Highly expressed in lung, heart, small colon, and pancreas.

I. TISSUE and VEGFR-2. VEGF-D first form an antiparallel homodimer.

I. Privi. Undergoes a complex proteolytic maturation which generates a variety of processed secreted forms with increased activity toward vegrR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer.

I. Inked by disulfide bonds before secretion. The fully processed bonds before secretion. The fully brocessed bonds before secretion. The fully brocessed bonds before secretion.

II. STMILARITY: Belongs to the PDGF/VEGF growth factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                           Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                   Stacker S.A., Stenvers K.L., Caesar C., Vitali A., Domagala T., Nice E.C., Rourdail S., Simpson R.J., Moritz R., Karpanen T., Alitalo K., Achen M.G.; "Biosynthesis of vascular endothelial growth factor-D involves
   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
                                                                                                                                                                                                                                                             PROCESSING, AND SEQUENCE OF 89-94; 100-105 AND 206-213.
MEDLINE-20011413; PubMed-10542248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; V12863; CAA73370.1; -.
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Gaps

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80.0%; Score 80; DB 1; Length 354; 93.8%; Pred. No. 5.9e-06; ive 0; Mismatches 1; Indels

0; Mismatches

N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
2048D769D735173E CRC64;

40444 MW;

354 AA;

145 155 185 287

BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).

2337 2233 2293 318 153 189 1189 1185 1185

301

142 146 136

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                                                                                                                                                  28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced
growth factor) (FIGF).
                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
                     28-FEB-2003 (Rel. 41, Created)
STANDARD;
                                                                                       Rattus norvegicus (Rat).
                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                     NCBI_TaxID=10116;
                                                                             FIGF OR VEGFD
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EMBL; AF014827; AAB66557.1; -.

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28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced growth factor) (FIGF)
      InterPro; F1902, 1ver.
InterPro; IPR004113;
InterPro; IPR000072; PD growth factor.
Pfam; PF00341; PDGF; 1.
Pfam; PF00341; PDGF; 1.
SNART; SN00141; PDGF; 1.
PROSITE; PS00249; PDGF 1; 1.
PROSITE; PS00249; PDGF 2; 1.
Angiogenesis; Mitogen; Growth factor; Glycoprotein; Signal; Repeat; Cleavage on pair of basic residues; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Orlandini M., Marconcini L., Ferruzzi R., Oliviero S.;
"Identification of a c-fos-induced gene that is related to the
platelet-derived growth factor/vascular endothelial growth factor
                                                                                                                                                                         POTENTIAL.
4 X 16 AA REPEATS OF C-X(10)-C-X-C-
X(1,3)-C.
                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamada Y., Nezu J.-I., Shimane M., Hirata Y.,
"Molecular cloning of a novel vascular endothelial growth factor,
                                                                                                                                                               VASCULAR ENDOTHELIAL GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                  .
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BY SIMILARITY.
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INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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1261AFA373596C00 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 1.7e-05;
                                                                                                                                                                                                               (APPROXIMATE)
                                                                                                                                                                                                                                                 4 (INCOMPLETE)
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                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE=Fibroblast;
MEDLINE=97030254; PubMed=8876195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97349118; PubMed=9205122;
                                                                                                                                                                                                                                                                                                                                                               37112 MW;
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126 ASELGKTTNTFFKPPC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ASELGKSTNTFCKPPC 17
                                                                                                                                                                                                                                                                                                                                                                                                 87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 87.5 es 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomics 42:483-488(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                        278
3317
1158
1194
1196
1141
1150
1150
                                                                                                                                                  93
                                                                                                                                                            210
326
317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        musculus (Mouse).
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 P15692; 1VPP
                                                                                                                                                                                                                                                                                                                                                             326 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FIGF OR VEGFD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VEGD_MOUSE
P97946;
                                                                                                                                                                                                                                                            DISULFID
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                                                                                                                                                                                                                                                                                                            DISULFID
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                                                                                                                                                                                                                                                                                                                                                CARBOHYD
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                                                                                                                                                            CHAIN
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                                                                                                                                                                                                                                                 REPEAT
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RA MEDLINE=2127641; PubMed=11279005;

RA Baldwin M.E., Catimel B., Nice E.C., Roufail S., Hall N.E.,

Baldwin M.E., Catimel B., Nice E.C., Roufail S., Hall N.E.,

Stenvers K.L., Karkkainen M.J., Alitalo K., Stacker S.A., Achen M.G.;

RT The specificity of receptor binding by vascular endothelial growth

RT factor d is different in mouse and man.";

RI J. Biol. Chem. 276:19166-19171(2001)

C. -I- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis

and endothelial cell growth, stimulating their proliferation and

CC and endothelial cell growth, stimulating their proliferation and

CC wind endothelial cell growth, stimulating their proliferation and

CC wessels. May function in the formation of the venous and lymphatic

CC vascular systems during embryogenesis, and also in the maintenance

CC differentiated lymphatic endothelium in adults. Binds and

CC differentiated lymphatic endothelium in adults. Binds and

CC -I- SUBGELLULAR LOCATION: Secreted.

CC -I- SUBGELLULAR LOCATION: Secreted.

CC -I- SUBGELLULAR SPECIFICITY: Highly expressed in fetal and adult lung.

CC -I- TISSUE SPECIFICITY: Highly expressed in fetal and adult lung.

CC -I- DEVELOPMENTAL STAGE: Expressed in a dynamic pattern in several

CC -I- DEVELOPMENTAL STAGE: Expressed in a dynamic pattern in several

CC -I- DEVELOPMENTAL STAGE: Expressed in a dynamic pattern in several

CC -I- DEVELOPMENTAL STAGE: Agraes of the embryo such as limb buds,

CC -I- DEVELOPMENTAL STAGE: Agraes of the embryo such as limb buds,

CC -I- DEVELOPMENTAL STAGE: Agraes of the embryo such as limb buds,

CC -I- DEVELOPMENTAL STAGE: Agraes of the embryo such as limb buds,

CC -I- DEVELOPMENTAL STAGE: Agraes of the embryo such as limb buds,

CC -I- DEVELOPMENTAL STAGE: Agraes of the embryo such as limb buds,

CC -I- DEVELOPMENTAL STAGE: Agraes of the embryo such as limb buds,

CC -I- DEVELOPMENTAL STAGE: Agraes of the embryo such as limb buds,

CC -I- DEVELOPMENTAL STAGE: Agraes of the embryo such as limb buds,

CC -I- DEVELOPMENTAL STAGE: Agraes of the embryo s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                      Avantaggiato V., Orlandini M., Acampora D., Oliviero S., Simeone A., "Embryonic expression pattern of the murine figf gene, a growth factor belonging to platelet-derived growth factor/vascular endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vertebral column.

INDUCTION: By the transcription factor c-fos.

NDUCTION: By the transcription factor c-fos.

For Undergoes a complex proteolytic maturation which generates a variety of processed secreted forms with increased activity toward VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer linked by disulfide bonds before secretion. The fully processed vEGF-D is composed mostly of two VEGF homology domains (VHDs) bound by non-covalent interactions (By similarity).

SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00249; PDGF 1; 1.
PROSITE; PSS0278; PDGF 2; 1.
Anglogenesis; Mitogen; Growth factor; Glycoprotein; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          o.
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4 X 16 AA REPEATS OF C-X(10)-C-X-C-
X(1,3)-C.
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VASCULAR ENDOTHELIAL GROWTH FACTOR
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GO; GO:000557; Fig.

GO; GO:0008083; Figrewth factor activity; IDA.

GO; GO:0008083; Figrewth factor activity; IDA.

GO; GO:0008283; P:cell proliferation; IDA.

InterPro; IPR004153; CXCXC_repeat.

InterPro; IPR004072; PD_growth_factor.

Pfam; PF03128; CXCXC; 2.

Promon; PD001629; PD growth_factor.

Promon; PD001629; PD growth_factor.

SMART; SM00141; PDGF; 1.
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2.
MEDLINE=98288130; PubMed=9622638;
                                                                                                                               Mech. Dev. 73:221-224 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X99572; CAA67892.1; -.
EMBL; D89628; BAA14002.1; -.
HSSP; P15692; IVPP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PMMA-2DPAGE; P97946; -.
                                                                                                      factor family."
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RESURENCE FROM N.A., AND SEQUENCE OF 108-126.

RAY MEDINE=9738482; PubMed=9247316;

RAY FITZ L.J., Morris J.C., Towler P., Long A., Burgess P., Greco R.,

RAY WANG J., Gassaway R., Nickbarg E., Kovacic S., Ciarletta A.,

Giannotti J., Finnerty H., Zollner R., Beier D.R., Leak L.V.,

RAY Turner K.J., Wood C.R.;

RAY Turner K.J., Wood C.R.;

RAY Turner K.J., Wood C.R.;

RAY Turner K.J., Wood C.R.;

RAY Turner K.J., Wood C.R.;

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RAY Turner K.J., Wood C.R.;

RAY Turner K.J., Wood C.R.;

RAY Turner K.J., Wood C.R.;

RAY Turner K.J., Wood C.R.;

RAY Turner Wood C.R.;

RAY Turner More Turner Wood Turner Will May Land L. More Toward

C. -1- TISSUE SPECIFICITY: Expressed in adult heart, brain, spleen, the perimetanephric, axillary and judular regions, and in the developing mesenterium. Expressed in adult heart, brain, spleen, wariety of processed secreted forms with increased activity toward

C. -1- TISSUE SPECIFICATION Turner Wood Turner Wood Turner Wood Turner Wood Turner Wood Turner Wood Turner
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15-JUL-1998 (Rel. 36, Last sequence update)
10-GCT-2003 (Rel. 42, Last annotation update)
10-GCT-2003 (Rel. 42, Last annotation update)
40-secular endothelial growth factor C precursor (VEGF-C) (Vascular endothelial growth factor related protein) (VRP) (Flt4 ligand) (Flt4-
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. ) (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "VEGFC receptor binding and pattern of expression with VEGFR-3 suggests a role in lymphatic vascular development."; Development 122:3829-3837(1996).
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Joukov V., Alitalo K.;
                                                                                                                                                                                                                                                  77.0%; Score 77; DB 1; Length 358; 87.5%; Pred. No. 1.9e-05; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                 6636B17FBF07037C CRC64;
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3.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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MEDLINE=97164697; PubMed=9012504;
                                                                                                                                                                                                                   40908 MW;
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                                                                                                                                                                                                                                                                                                     14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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358 AA;
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                                                                                                                                                                                                                                                                              Local Similarity
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                                                                      DISULFID
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                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-00T-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Vascular endothelial growth factor C precursor (VEGF-C) (Vascular endothelial growth factor related protein) (VRP) (Flt4 ligand) (Flt4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
VEGF-C first form an antiparallel homodimer linked by disulfide bonds. Before secretion, a cleavage occurs between arg-227 and ser-228 producing an heterotetramer. The next extracellular step of the processing removes the N-terminal propeptide. Finally the mature VEGF-C is composed mostly of two VEGF homology domains (VHDs) bound by non-covalent interactions (By similarity). SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
                                                                                                                                                                                                                                                                                                                                                                   Pfam; PP00341; FUGE; 1.

PRINTS; PR00438; GECYSKNOT.

PRODOM; PD001629; PD growth_factor; 1.

SMART; SM00141; PDGF; 1.

PROSITE; PS00249; PDGF 1; 1.

PROSITE; PS50278; PDGF 2; 1.

Anglogenesis; Mitogen; Growth factor; Glycoprotein; Signal; Repeat; Claavage on pair of basic residues; Multigene family.

BY SIMILARITY.
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4 X 16 AA REPEATS OF C-X(10)-C-X-C-X(1,3)-C.
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                    MGD; MGI:109124; Vegfc.
InterPro; IPR004153; CXCXC_repeat.
InterPro; IPR002400; GF_CYSKnot.
InterPro; IPR00022; PD_growth_factor.
Pfam; PF03128; CXCXC; 5.
Pfam; PF00341; PDGF; 1.
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71.4%;
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Best Local Similarity 71.4
Matches 10; Conservative
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SUBUNIT: Homodimer; non-covalent and antiparallel.

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L Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                Joukov V., Pajusola K., Kaapainen A., Chilov D., Lahtinen I., Kukk E., Saksela O., Kalkkinen N., Alitalo K.; A notel vascular endothelial growth factor, VEGF-C, is a ligand for the Flt4 (VEGFR-3) and KDR (VEGFR-2) receptor tyrosine kinases."; EMBO J. 15:290-298(1996).
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"Proteolytic processing regulates receptor specificity and activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 32-41; 112-121 AND 228-233, AND MUTAGENESIS OF ARG-227. MEDLINE=97377029; PubMed=9233800;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Glial tumor;
MEDLINE=96312526; PubMed=8700872;
MEDLINE=96312526; PubMed=8700872;
Lee J., Gray A., Yuan J., Luoh S..M., Avraham H., Wood W.I.;
"Vascular endothelial growth factor-related protein: a ligand and specific activator of the tyrosine kinase receptor Flt4.";
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE=97388482; PubMed=9247316;
Fitz L.J., Morris J.C., Towler P., Long A., Burgess P., Greco Fitz L.J., Morsis J.C., Towler P., Long A., Burgess P., Granletta A., Giannotti J., Finnerty H., Zollner R., Beier D.R., Leak L.V., Turner K.J., Wood C.R., "Characterization G.R." murine Flt4 ligand/VEGF-C.";
                                                                                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE OF 103-120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                               MEDLINE=96178224; PubMed=8617204;
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                                                                                NCBI_TaxID=9606;
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-: SUBGRELLUIAN LOCARION. Secreted.
-: TISSUE SPECIFICITY: Spleen, lymph node, thymus, appendix, bone marrow, heart, placenta, ovary, skeletal muscle, prostate, testis, colon and small intestine and fetal liver, lung and kidney, but not in peripheral blood lymphocyte.
-: PTM: Undergoes a complex proteolytic maturation which generates a variety of processed secreted forms with increased activity toward VEGTR-3, but only the fully processed form could activate VEGFR-2. VEGTR-3, but only the fully processed form could activate VEGFR-2. VEGTR-3, but only the fully processed form could activate VEGFR-2. VEGFR-3, but only the fully brocessed form could activate VEGFR-2. VEGFR-3, but only the fully brocessed form could activate VEGFR-2. VEGFR-3, but only the fully brocessed cocurs between arg-22 and set-228 producing an heterotetramer. The next extracellular step of the processing removes the N-terminal propeptide. Finally the mature VEGF-C is composed mosely of two VEGF homology domains (VHDs) bound by non-covalent interactions.
                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PROSITE; PS50278; PDGF 2; 1.
Angiogenesis; Mitogen; Growth factor; Glycoprotein; Signal; Repeat; Cleavage on pair of basic residues; Multigene family.
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BY SIMILARITY.

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INTERCHAIN (BY SIMILARITY).

INTERCHAIN (BY SIMILARITY).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
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GO; GO:000284; P:positive regulation of cell proliferation; TAS.
GO; GO:0007165; P:signal transduction; TAS.
GO; GO:0007165; P:signal transduction; TAS.
InterPro; IPR004153; CXCXC_repeat.
InterPro; IPR00400; GF cysknot.
InterPro; IPR000072; PD_growth_factor.
Pfam; PF03128; CXCXC_; FP
Pfam; PF03141; PDGF; 1.
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VASCULAR ENDOTHELIAL GROWTH FACTOR
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Pred. No. 0.034;
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ProDom; PD001629; PD_growth_factor; 1.
SMART; SM00141; PDGF; 1.
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EMBL; U43142; AAA85214.1; -.
EMBL; U58111; AAB02909.1; -.
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71.4%;
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HSSP; P15692; 1VPP.
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Best Local Similarity
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KRA KUNBEL F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

KRA KUNSE F., Ogasawara N., Moszer I., Albertini A.M., Borchert S.,

RA Aceved V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

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RA Guiseppi G., Wasahara Y., Klaerr-Blanchard M., Klein C.,

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RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

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RA Presecan B., Pujic P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Presecan B., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,

RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,

Sorotin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,

RA Takeuchi M., Tamakoshi A., Tanaka T., Tarebmaru P., Tosmoni A.,

RA Takeuchi M., Tamakoshi A., Tanaka T., Tarebmaru P., Tosmoni A.,

RA Voshida K., Yoshikawa H.F., Zumstein E., Woshikawa H., Danchin A.,

RA Winters P., Wipat A., Yamamoto et the Gram-positive bacterium Bacillus

RH H. H. Wallin R., Schleiber E., Woshikawa H., Danchin A.,

RH H. H. Wallin R., Soshikawa H.F., Zumstein R., Yoshikawa H., Danchin A.,

RH H. H. Wallin R., Schleiber E., Wolleiber E., Wolleiber E., Woshikawa H.F., Zumstein B., Soshikawa H.F., Zumstein B., Yoshikawa H.F., Zumstein B., Soshikawa H.
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Morohoshi F., Hayashi K., Munakata N.;
"Molecular analysis of Bacillus subtilis ada mutants deficient in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haga K., Liu H., Yasumoto K., Takahashi H., Yoshikawa H.;
"Sequence analysis of the 70kb region between 17 and 23 degree of the
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-91016831; PubMed-2120677; Munakata N.; Munchoshi F., Hayashi K., Munakata N.; Munakata N.; Bacillus subtilis ada operon encodes two DNA alkyltransferases."; Nucleic Acids Res. 18:5473-5480(1990).
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     Indels
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     Mismatches
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143 EFGVATNTFFKPPC 156
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     Conservative
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Bacillus subtilis.
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P19219;
     10;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PROSITE; P80124; HTH ARAC FAMILY 2; 1.

DNA repair; Transcription regulation; Transferase; Methyltransferase; Activator; DNA-binding; Metal-binding; Zinc; Complete proteome.

METAL 54 54 51 SINC (BY SIMILARITY).

METAL 58 58 ZINC (BY SIMILARITY).

METAL 85 88 ZINC (BY SIMILARITY).

METAL 88 88 ZINC (BY SIMILARITY).

METAL 88 88 ZINC (BY SIMILARITY).

ACT 51 88 8 ZINC (BY SIMILARITY).

ACT 51 88 88 ACCEPTOR FOR METHYL FROM PHOSPHOTRIESTER.
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MEDINE=20181126; PubMed=10718198;
Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XVI.
The complete sequences of 150 new cDNA clones from brain which code
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                                               PUNCTION: METHYLDHOSPHOTRIBSTER-DNA ALKYLTRANSFERASE IS ONE OF FUNCTION: METHYLDHOSPHOTRIBSTER-DNA ALKYLTRANSFERASE IS ONE OF TWO GENES REQUIRED FOR THE ADAPTIVE RESPONSE OF BACTERIA TO ALKYLATING AGENTS. IT ACCEPTS A METHYL GROUP FROM METHYLPHOSPHOTRIBSTERS AND THEN ACTS AS A TRANSCRIPTIONAL ACTIVATOR OF THE
                                                                                                                                                                                                                                COFACTOR: One zinc ion per subunit (By similarity). SIMILARITY: TO THE N-TERMINAL REGION OF E.COLI ADA PROTEIN AND THE C-TERMINAL REGION OF THE ARAC/XYLS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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920931082527EC27 CRC64;
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adaptive response to simple alkylating agents.";
J. Bacteriol. 173:7834-7840(1991).
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical protein KIAA1383.
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EMBL, Z99104; CAB11957.1;
- PIR; S1488; XUBSMM.
HSSP, P06134; IADN.
SUBCTLIST; BG10166; adaA.
InterPro; IPR004026; Ada Zn bind.
InterPro; IPR00005; HTHĀraē.
Pfam; PF02805; Ada Zn binding; IPR
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24299 MW;
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SMART; SM00342; HTH_ARAC; 1.
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Best Local Similarity
Local 8; Conserve
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211 AA;
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Sogai T.;
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TISSUBE-Testis;

A Strausberger R.L. Feingold B.A. Grouse L.H., Derge J.G.,

A Strausberg R.L. Feingold B.A. Grouse L.H., Derge J.G.,

A Kluusner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altechul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,

BA Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

R. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

R. Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hillyk S.W.,

R. Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hillyk S.W.,

R. Hillalon D.K., Muzzhy D.W., Sodergren B.J., Lu X., Gibbs R.A.,

R. Hatting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R. Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

R. Butterfield Y.S.N., Krzywinski M.I., Saalska U., Smailus D.E.,

R. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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Pred. No. 7.6;
                                                                                                                                                                   to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 905 AA; 100344 MW; B02FBD0EDAD78491 CRC64;
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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   for large proteins in vitro.";
DNA Res. 7:65-73(2000).
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TISSUE=Brain;
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A MEDLINE=22388557; PubMed=12477932;

RA MEDLINE=22388557; PubMed=12477932;

RA Altaner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altaner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altechul S.F., Zeeberg B., Butcow K.H., Schaefer C.F., Bhat N.K.,

RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

RA Bitchehov L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brank S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muxny D.W., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.N.,

R Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R Generation and initial analysis of more than 15,000 full-length

R Proc. Natl. Acad. Sci. U.S.P. 99:16899-16903(2002).
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                  s:
Kim K.I., Baek S.H., Jeon Y.-J., Nishimori S., Suzuki T., Uchida S., Shimbara N., Saitoh H., Tanaka K., Chung C.H., "A new SUWO-1-specific protease, SUSP1, that is highly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang Y.-G.; "Identification of FKSG6, a novel protein with protease activity."; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XI. The complete sequences of 100 new cDNA clones from brain which code
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 29-1112 FROM N.A. (ISOFORM 1), AND VARIANT CYS-1106.
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DNA Res. 5:277-286(1998).
-!- FUNCTION: Protease that releases SUMO-1 from its precursor
                                                                                                                                                                                                                                                                                                                                               Gong L., Yeh E.T.H.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "NEDO human cDNA sequencing project.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohara O., Suyama M., Nagase T., Ishikawa K., Kikuno R., Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT CYS-1106.
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-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-692 FROM N.A. (ISOFORM 2).
                                                                                                                                                                                Biol. Chem. 275:14102-14106(2000).
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                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                       reproductive organs."
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                                                                                                                                                                                                                                                                                                           TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Testis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rissum=Brain;
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             FUNCTION: May play a role in cell-cell and cell-matrix interactions. May contribute to various neuronal mechanisms in the
                                                                     -:- SUBCELLUIAR LOCATION: Secreted, extracellular matrix.
-:- TISSUB SPECIFICITY: Predominantly expressed in the postsynaptic area of pyramidal neurons.
-:- PTM: Contains chrondroitin sulfate and heparan sulfate 0-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Embryo;
MEDIINE=91093131; PubMed=1985896;
Ardelt W., Mikulski S.M., Shogen K.;
Anino acid sequence of an anti-tumor protein from Rana pipiens
ocytes and early embryos. Homology to pancreatic ribonucleases.";
J. Biol. Chem. 266:245-251(1991).
                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:105371; Spock1.
InterPro; IPR002350; kazal.
InterPro; IPR00716; Thyroglobulin_1.
Pfam; PF00086; thyroglobulin_1; 1.
Pfam; PF00086; thyroglobulin_1; 1.
SMART; SM00210; KAZAL; 1.
SMART; SM00210; Tr; 1.
EXCATE; PS00484; THYROGLOBULIN 1; 1.
EXCATACELLULAR matrix; Proteoglycan; Heparan sulfate; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-FBE-1994 (Rel. 28, Last sequence update)
28-FBE-3003 (Rel. 41, Last annotation update)
P-30 protein (EC 3.1.27.-) (Onconase).
Rana piptens (Northern leopard frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KAZAL-LIKE.
THYROGLOBULIN TYPE-1.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
C-LINKED (GLYCOSAMINOGLYCAN) (HOUSEN)
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Pred. No. 5.4;
                                                                                                                                               oligosaccharides.
-!- SIMILARITY: Contains 1 Kazal-like domain.
-!- SIMILARITY: Contains 1 thyroglobulin type-I domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     818C30313F8AC0F6 CRC64;
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Biol. Chem. 271:4373-4380(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.0%;
50.0%;
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                                                     central nervous system.
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162
183
386
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442
183
379
100
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Best Local Similarity
Free 8; Conserva
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386
391
342 AA;
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P22069;
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SIGNAL
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                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profilt institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
                                                       Note=No experimental confirmation available; ITSSUB SPECIFICITY: Highly expressed in reproductive organs, such as testis, ovary and prostate. SIMILARITY: Belongs to peptidase family C48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BALB/C; TISSUE=Brain; MEDLINE=96224019; PubMed=8626787; Bonnet F., Perin J.-P., Charbonnier F., Camuzat A., Roussel G., Nussbaum J.L., Alliel P.M.; Ristructure and cellular distribution of mouse brain testican. Association with the postsynaptic area of hippocampus pyramidal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003653; Peptidase_C48.
Pfam; PP02902; Peptidase_C48; I.
PROSITE; PS50600; ULP PRÖTEASE; I.
Hydrolase; Protease; Thiol protease; Ubl conjugation pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /FTId=VSP 005274.
Y -> C (in dbSNP:9250).
/FTId=VAR 016096.
T -> M (IN REF. 1, 6 AND 7).
D -> V (IN REF. 5).
Q -> E (IN REF. 1, 4, 6 AND 7).
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Pred. No. 9.3;
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BY SIMILARITY.
BY SIMILARITY.
Missing (in isoform 2).
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28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
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3; Mismatches
                                         IsoId=Q9GZR1-2; Sequence=VSP_005274;
   lsoId=Q9GZR1-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alternative splicing, Polymorphism.
DOMAIN 666 1112 PROTEASB.
ACT SITE 765 BY SIMILA
ACT_SITE 917 917 BY SIMILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Testican-1 precursor (SPOCK protein). SPOCK OR SPOCK1 OR TICN1.
                                                                                                                                                                                                                                                                                                                                                              EMBL, BC028583; AAH28583.1; -.
EMBL, AKO96455; BAC04794.1; -.
EMBL, AB018340; BAA34517.2; ALT_INIT.
MEROPS; C48.004; -.
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954 CSSEIGOWHLKPTICKOPC 972
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                                                                                                                                                                                                                                                                                                          EMBL; AF196304; AAF04852.1; -. EMBL; AF307849; AAG29831.1; -. EMBL; AF306508; AAG30253.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 46.0%;
Similarity 47.4%;
9; Conservative
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ID TIC1 MOUSE
AC Q62288;
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ACT_SITE
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EX26_ARATH
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                                                                                                                                                                          MEDLINE=94166079; PubMed=8120892; Mosimann S.C., Ardelt W., James M.N.G.; Mosimann S.C., Ardelt W., James M.N.G.; Mosimann S.C., Ardelt W., James M.N.G.; Mosimann in the propose with anti-tumor activity."; J. Mol. Biol. 236.1141-1153 (1994)
-!- FUNCTION: Basic protein with antiproliferative/cytotoxic activity against several tumor cell lines in vitro, as well as antitumor in vivo. It exhibits a ribonuclease-like activity against high
                                                                                                                                                                                                                                                                                                           molecular weight ribosomal RNA.
DEVELOPMENTAL STAGE: Early embryos (up to four blastomere stage).
SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                  "Comparative molecular modeling and crystallization of P-30 protein: a novel antitumor protein of Rana pipiens occytes and early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
[2]
3D-STRUCTURE MODELING.
MEDLINE=93066156; PubMed=1438177;
Mosimann S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative alpha-expansin 22 precursor (At-EXP22) (AtEx22) (Ath-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PYRROLIDONE CARBOXYLIC ACID.
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                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM0092; RNASE PC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; 3D-structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.0%; Score 43; DB 1; 61.5%; Pred. No. 2.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
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                                                                                                                                                                                                                                                                                                                                                           PDB; IONC; 31-JAN-94.
InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pyrrolidone carboxylic acid.
                                                                                                                                  Proteins 14:392-400(1992).
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es 8; Conserv
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EX22_ARATH
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rmatics and the EMBL outstation
There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Causes loosening and extension of plant cell walls by disrupting noncovalent bonding between cellulose microfibrils and matrix glucans. No enzymatic activity has been found (By
Exphlpha-1.15).

EXPEZ-OR ATSG39270 OR K3K3.18 OR K3K3.120.

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -! SINIARITY).
-! SUBCELULAR LOCATION: Cell-wall bound.
-! SIMILARITY: Belongs to the expansin family.
-!- SIMILARITY: Contains 1 expansin-like EG45 domain.
-!- SIMILARITY: Contains 1 expansin-like CBD domain.
-!- GAUTION: Ref. 1 sequence differs from that shown due to erroneous gene model prediction.
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE=9834145; PubMed=9679202;
Kaneko T., Kotani H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                           "Structural analysis of Arabidopsis thaliana chromosome 5. V. features of the regions of 1,381,565 bp covered by twenty one physically assigned Pl and TAC clones.";
DNA Res. 5:131-145(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prodom; PD002179; Expan Lol pl C; 1.
PROSITE; PS50843; EXPANSIN CBD; 1.
PROSITE; PS50842; EXPANSIN EG45; 1.
Hypothetical protein; Cell wall; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no resuse by non-profit institutions as long as its content
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EXPANSIN-LIKE CBD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WWW="http://www.bio.psu.edu/expansins/".
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(Rel. 41, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- DATABASE: NĀME=EXPANSIN homepage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR007112; Expan endogl.
InterPro; IPR007118; Expan endogl.
InterPro; IPR007118; Expan_Lol_pI.
InterPro; IPR007117; Expan_Lol_pI.
Pfam; PF01357; Pollen allergen; I.
PRINTS; PR01225; EXPANSNFAMLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cosgrove D.J.;
Unpublished observations (DEC-2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONCEPTUAL TRANSLATION
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
1-OCT-2003 (Rel. 42, Last annotation update)
4-hydroxy-3-methylbut-2-enyl diphosphate reductase (BC 1.17.1.2).
ISPH OR LYTB OR BUL147.
Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                          "Addition: Converts 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate into isopentenyl diphosphate (IPP) and dimethylallyl diphosphate (DMAPP) (By similarity).

-!-CATALYTIC ACTIVITY: Isopentenyl diphosphate + NAD(P)(+) + H(2)O = (E)-4-hydroxy-3-methylbut-2-en-1-yl diphosphate + NAD(P)H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spermatophyta, Magnoliophyta, eudicóryledons, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta
                                                                                                                                                                                                                                                                                                                       MEDDINE=20445173; PubMed=10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids
                                                                                                                                                                     Bacteria; Froteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Buchnera.
NCBI_TaxID=118099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=cv. Columbia;
Samac D.A., Hironaka C.M., Yallaly P.E., Shah D.M.;
"Isolation and characterization of the genes encoding basic and
acidic chitinase in Arabidopsis thaliana.";
Plant Physiol. 93:907-914(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     iosynthesis; Complete proteome; Oxidoreductase; NADP. 319 AA; 35741 MW; 69D8AFCC12DD09B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41.0%; Score 41; DB 1; Length 319; 66.7%; Pred. No. 18; 3; Indels ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1991 (Rel. 17, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Basic endochitinase precursor (EC 3.2.1.14)
AT3612500 OR TZE22.18 OR TZE22 119 OR MCG3.34.
Arabidopsis thaliana (Mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      322 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (last) step.
-!- SIMILARITY: Belongs to the ispH family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGREAMS; TIGRO0216; ispH lytB; 1.
Isoprene biosynthesis; Complete pro
SEQUENCE 319 AA; 35741 MW; 69D8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AP001118; BAB12865.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1990 (Rel. 16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAP; MF 00191; -; 1.
InterPro; IPR003451; LytB.
Pfam; PF02401; LYTB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 AÉLGKETGTFTK 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 66.7
nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 SELGKSTNTFCK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                      Buchnera sp. APS.";
Nature 407:81-86(2000).
                                                                                                                                                         symbiotic bacterium)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                     STRAIN=Tokyo 1998;
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHIT ARATH P19171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
CHIT ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                       "Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence features of the regions of 1,381,565 bp covered by twenty one physically assigned Pl and TAC clones.";
DNA Res. 5:131-145(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished observations (DEC-2001).
-!- FUNCTION: Causes loosening and extension of plant cell walls by disrupting noncovalent bonding between cellulose microfibrils and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1. SUBCELLULAR LOCATION: Cell-wall bound.
-1. SIMILARITY: Belongs to the expansin family.
-1. SIMILARITY: Contains 1 expansin-like EG45 domain.
-1. SIMILARITY: Contains 1 expansin-like EG45 domain.
-1. CAUTION: Ref.1 sequence differs from that shown due to erroneous gene model preddiction.
-1. DATABASE: NAME=EXPANSIN homepage;
                                                                                                        Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                   STRAIN=cv. Columbia;
MEDLINE=98344145; PubMed=9679202;
Kaneko T., Kotani H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                   Putative alpha-expansin 26 precursor (At-EXP26) (AtBx26) (Ath-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            matrix glucans. No enzymatic activity has been found (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AB010694; BAB09384.1; -.

InterPro; IPR007112; Expan_endogl.

InterPro; IPR007118; Expan_Lol_pl.

InterPro; IPR007118; Expan_Lol_pl.

PR007118; PR001215; EXPANSNFAMLY.

PRINTS; PR01225; EXPANSNFAMLY.

PRODGM; PSCO843; EXPANSIN CBD; 1.

PROSTIE; PSCO842; EXPANSIN CBD; 1.

PROSTIE; PSCO842; EXPANSIN EG45; 1.

Hypochetical protein; Cell wall; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43.0%; Score 43; DB 1; Length 279; 37.5%; Pred. No. 7.5; 6; Indels ive 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUTATIVE ALPHA-EXPANSIN 26.
EXPANSIN-LIKE BG45.
EXPANSIN-LIKE CBD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5053E7CB497E47C4 CRC64;
               Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WWW="http://www.bio.psu.edu/expansins/".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 319 AA.
                                                                                      EXP26 OR AT5G39290 OR K3K3.20 OR K3K3 140.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30980 MW;
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186
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                 28-FEB-2003 (Rel. 41,
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                            NCBI TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity)
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ID ISPH BUCAI
AC P57247;
                                                                                                                                                                                                                                                                                                                                                             Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cosgrove
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SIGNAL DOMAIN DOMAIN

RESULT 13

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Gaps

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Glaser P., Prangeul L., Buchrisser C., Rusniok C., Amend A.,
Glaser P., Frangeul L., Buchrisser C., Rusniok C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Andrbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominquez-Bernal G., Duchaud E., Durant L., Dussurget O.,
B. Brtian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
A Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Mattournam A., Mata Vicente J., NG E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
A varquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
Comparative genomics of Listeria species.",
Science 294:849-8522(201).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- CATALYTIC ACTIVITY: Arp + acetate = ADP + acetyl phosphate.
-:- PATHWAY: Conversion of acetate to acetyl-CoA; first step.
-:- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-:- SIMILARITY: Belongs to the acetokinase family.
                                                                                                       Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
             28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Acetate kinase 2 (BC 2.7.2.1) (Acetokinase 2)
                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-CLIP 11262 / Serovar Ga;
MEDLINE-21537279; PubMed=11679669;
                                                                    ACKA2 OR LIN1132
                                                                                         Listeria innocua.
                                                                                                                      NCBI_TaxID=1642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Matches
             à
                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license&ib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REMEL; AP002047; BAB03157.1; ---
REMEL; AP002047; BAB03157.1; ---
REMEL; AP002047; BAB03157.1; ---
REMESP: P23951; 2BAA.

InterPro; IPR001022; Chitin binding 1.

RICHERT: AP00182; Chitin binding 1.

REMEL; AP00187; Chitin binding 1.

REMEL; PR00187; Chitin binding 1; 1.

REMEL; PR00187; Chitin binding 1; 1.

REMEL; PR00187; Chitin binding 1; 1.

REMEL; PR00170; Chitin binding 1; 1.

REMEL; PS00170; Chitin binding 1; 1.

REMEL; PS00170; Chitin binding 1; 1.

REMEL; PS00170; Chitin BIND 1; 1.

REMEL; PS00177; CHITINASE 19; 1.

REMEL; PS00774; CHITINASE 19; 1.

REMEL; PS00774; CHITINASE 19; 1.

REMEL; PS00774; CHITINASE 19; 1.

REMEL; PS00774; CHITINASE 19; 1.

REMEL; PS00774; CHITINASE 19; 1.

REMEL; PS00774; CHITINASE 19; 1.

REMEL; PS00774; CHITINASE 19; 1.
                                                                                                                                            FRES. 7:217-221(2000).
FUNCTION: This protein functions as a defense against chitin containing fungal pathogens.
CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of Nacetyl-D-glucosamine polymers of chitin.
SUBCELLULAR LOCATION: Vacuolar and protoplast.
IISSUE SPECIFCITY: High constitutive level in roots with lower levels in leaves and flowering shoots.
INDUCTION: Ethylene induces high levels of systemic expression of basic chitinase with expression increasing with plant age.
SIMILARITY: Belongs to chitinase class IA (family 19 of glycosyl
                 SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
STRAIN=cv. Columbia;
Kanelv T., Katoh T., Sato S., Nakamura A., Asamizu E., Tabata S.;
Kaneko T., Katoh T., Sato S., Nakamura A., Asamizu E., Tabata S.;
"Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the 4,251,695 bp regions covered by 90 Pl, TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASIC ENDOCHITINASE.
REMOVED IN MATURE FORM (PROBABLE).
CHITIN-BINDING TYPE-1.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Contains 1 chitin-binding type-1 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C9AFFE4C544FCCD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M38240; AAA32769.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34609 MW;
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50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              322 AA;
                                                                                                                                  BAC clones.";
                                                                                                                                                                                                                                                                                                                                                          hydrolases)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41, DB 1; Length 397;
Pred. No. 23;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5822544EF92CBF51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5, 2004, 09:56:05
                                                                                                                                                    entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00811; Acetate kinase; 1.
PRINTS; PR00471; ACETATEKNASE.
TIGRFAMS; TIGR00116; ack3; 1.
PROSITE; PS01076; ACETATE KINASE 1; 1.
PROSITE; PS01076; ACETATE KINASE 2; 1.
Transferase; Kinase; Complete proceome.
SEQUENCE 397 AA; 43115 MW; 58225441
                                                                                                                                                                                                                                                                                                            ListiList, LIN01132; -.
MAMAP, MF 00020; -; 1.
INTERFO: IPR000890; Acetate_kin.
InterPro; IPR004372; AckA.
                                                                                                                                                                                                                                           EMBL; AL596167; CAC96363.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 72.7%;
8; Conservative
                                                                                                                                                                                                                                                                          PIR; AC1574; AC1574.
ListiList; LIN01132; -.
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Job time : 8.72727 secs
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Gaps

7

6; Indels

1; Mismatches Pred. No. 19;

1 CASELGKSTNT--FCKPP 16

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Local Similarity 50.0 les 9; Conservative

Matches

54

37 CCSEFGWCGNTEPYCKOP

397 AA.

PRT;

STANDARD;

ACK2_LISIN ID ACK2_LISIN AC Q92CN9; DT 28-FEB-2003

RESULT 15

Q92CN9; 28-FEB-2003 (Rel. 41, Created)

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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September 5, 2004, 09:46:09; Search time 38.4646 Seconds (without alignments) 139.448 Million cell updates/sec Run on:

US-09-761-636A-8 100 1 CASELGKSTNTFCKPPC 17 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1017041 seqs, 315518202 residues Searched:

1017041 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL_25:*
1: Sp_archea:*
2: Sp_bacteria:*
3: sp_tungi:*
4: Sp_tungi:*
5: Sp_tungi:*
5: Sp_tungi:*
7: Sp_manmal:*
7: Sp_manmal:*
7: Sp_manmal:*
7: Sp_phage:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	091ze4 rattus norv	OBaad7 aallus aall				Ogys50 hos tamps	07t3i6 brachydanio	ניניים אליים איש אליים פרע	OBbis7 mis miscuin		D91t18 arabidoneis	O81791 arabidonais	O18118 Caphorhabdi	ORIVITA DECISIONAL	Ogmand Janasans Al	Q81jj8 bacillus an
SUMMARIES	ID	091ZE4	Q8QGD7	91ZH6	091ZE3	057352	09X820	07T3I6	09CUD6	08BJS7	091878	O9LTJ8	08L791	018118	O81WU7	OSMD06	081338
	DB	11	13	11	11	13	9	13	11	11	13	10	10	Ŋ	16	œ	16
	Query Aatch Length DB	326	252	326	415	418	420	396	888	891	127	746	746	330	198	326	605
оķо	Query	77.0	61.0	59.0	59.0	59.0	59.0	51.5	50.0	50.0	49.0	48.5	48.5	48.0	46.0	46.0	46.0
	Score	77	61	59	59	59	59	51.5	50	20	49	48.5	48.5	48	46	46	46
	Result No.	н	7	m	4	S	ø	7	œ	σ	10	11	12	13	14	15	16

O814iO bacillus ce	pyrobacul		_					U	O8ibs4 plasmodium							09v111 drosophila	026566 schistosoma	O9zkw0 helicobacte	Oguvx5 rana pipien		008001 saccharomyc		0967zl trypanosoma	091kw0 lycopersico			O90944 pheumocysti	
6 081410	7 Q8ZTL2	6 Q81A51	1 Q8BM07	0 Q9C6R6	1 Q8BM19	0 09C6F7	1 08BK03	0	_	Q9VE57	_	16 Q8D4T1	10 Q9FHK1	0 09FLD9	•	_			13 Q8UVX5	6 Q8R6T0	008001	096803	096721	O Q9LKWO	09XYV5	0 P93680	09P944	044341
605 1	86 1	198 1	364 1	367 1	367 1	371 1	439 1	621 5	1036 5		193 5	•		677 1	1189 5	1189 5		•	127 1	•	693 3	849 4	997 5	175 1	288 5	326 1	1011 3	1428 5
46.0	45.0	45.0	45.0	45.0	45.0	45.0	45.0	44.5	44.5	44.0	44.0	44.0	44.0	44.0	44.0	44.0	44.0	43.0	43.0	43.0	43.0	43.0	43.0	42.0	42.0	42.0	42.0	42.0
46	45	45	45	45	45	45	45	44.5	44.5	44	4	44	44	44	44	44	44	43	43	43	43	43	43	42	42	42	42	42
17	18	19	20	21			24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

Indels , i 14; Conservative 1; Mismatches Matches

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Gaps

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2 ASELGKSTNTFCKPPC

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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley;
Kirkin V., Mazitschek R., Krishnan J., Steffen A., Waltenberger J.,
Pepper M.S., Glannis A., Sleeman J.P.;
"Characterization of indolinones which specifically inhibit VEGF-C-and
VEGF-D-induced activation of VEGFR-3 but not VEGFR-2.";
EMEL, AV032729; AAK96009.1;
EMEL, AV032729; AAK96009.1;
GO; GO:0016000; C:membrane; IEA.
GO; GO:0008151; P:cell growth and/or maintenance; IEA.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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Pred. No. 0.042;
1; Mismatches 3; Indels
                                                                                                                                                              Query Match

S9.0%; Score 59; DB 11; Length 326;
Best Local Similarity 71.4%; Pred. No. 0.033;
Matches 10; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SMULALI, FLOCK, L.
PROSITE; PS02249; PDGF L];
PROSITE; PS50278; PDGF L];
CERRINGE 415 AA; 46397 MW; 1EB677F5B260A525 CRC64;
                                                                                                                                  326 AA; 36826 MW; DOB2772C77836914 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   057352;
01-UJN-1998 (TrEMBLrel. 06, Created)
01-UJN-1998 (TrEMBLrel. 06, Last sequence update)
01-UJN-2003 (TrEMBLrel. 24, Last annotation update)
Vascular endothelial growth factor C precursor.
                                                                                                                                                                                                                                                                                                                                                                  Q91ZE3;
0-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     418 AA
                                                                                                                                                                                                                                                                                                                                                   PRT; 415 AA.
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InterPro; IPR004153; CXCXC repeat.
InterPro; IPR0000072; PD_growth_factor.
Pfam; PF001128; CXCXC; 5
Pfam; PF00141; PDGF; 1.
PRINTS; PR00438; GFCXSXNOT.
ProDom; PD0001629; PD_growth_factor; 1.
SMART; SM00141; PDGF; 1.
Pfam; PF03128; CXCXC; 5.
Pfam; PF00341; PDGF; 1.
PRINTS; PR00438; GFCYSKNOT.
ProDom; PD001629; PD_growth_factor; 1.
SMART; SM00141; PDGF; 1.
PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 71.4%;
Matches 10; Conservative
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                                                                                                                                                                                                                                 4 ELGKSTNTFCKPPC 17
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50 EFGAATNTFFKPPC 63
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                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                     NON TER
SEQUENCE
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VEGF-C.

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Length 420; 3; Indels

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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae, Danio.
NCBI_TaxID=7955,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Adult male testis cDNA, RIKEN full-length enriched library,
clone:4933403G14 product:hypothetical serine-rich region containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                             VASCULAR ENDOTHELIAL GROWTH FACTOR
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STRAIN=C57BL/6J; TISSUE=Testis;
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.5%; Score 51.5; DB 13; Length 396; 58.8%; Pred. No. 0.9; 1; Indels 3; Mismatches 1; Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Olofesson B., Ober E.A., Makinen T., Jin S.-W., Shoji W., Koh Alitalo K., Stainier D.Y.R., "Vascular endothelial growth factor C regulates endodermal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 morphogenesis in zebrafish.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF466147; AAP44161.1;
SEQUENCE 396 AA; 45287 MW; C20F9B3F0307D7C1 CRC64;
                                                                                                                                                                                                             58BA84317A3C8E2D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
                                                                                                                                                                                                                                               59.0%; Score 59; DB 6; 71.4%; Pred. No. 0.043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        396 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence up
01-0CT-2003 (TrEMBLrel. 25, Last annotation
Vascular endothelial growth factor C
Brachydanio rerio (Zebrafish) (Danio rerio).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           888 AA.
                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein, full insert sequence (Fragment)
4933403G14RIK.
                                                                                                                                                                          POTENTIAL
                     Pfam; PF03128; CXCXC; 5...
Pfam; PF00341; PDGF; 1.
PRINTS; PR00438; GFCYSKNOT.
ProDom; PD001629; PD growth_factor; 1.
SMART; SM00141; PDGF; 1.
     InterPro; IPR000072; PD_growth_factor.
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                                                                                                                                                                                                           46681 MW;
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                                                                                                              PROSITE; PS00249; PDGF 1; 1.
PROSITE; PS50278; PDGF 2; 1.
                                                                                                                                                                                                                                                                                                                                                    144 EFGAATNTFFKPPC 157
                                                                                                                                                                                                                                                                                                                         4 ELGKSTNTFCKPPC 17
                                                                                                                                                                                                                                           Query Match
Best Local Similarity 71.4
Matches 10; Conservative
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                                                                                                                                                                                                           420 AA;
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les 10; Conserv
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Q7T316;
                                                                                                                                                    Signal.
SIGNAL
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             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                     MEDLINE=98167900; PubMed=9435294;
Bichmann A., Corbel C., Jaffredo T., Breant V., Joukov V., Kumar V.,
Alitalo K., Le Douarin N.M.;
"Avian VEGF-C: cloning, embryonic expression pattern and stimulation
of the differentiation of VEGFR2 expressing endothelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bovoidea; MCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL,
VASCULAR ENDOTHELIAL GROWTH FACTOR
099BFCC79151BF2B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 59; DB 13; Length 418;
Pred. No. 0.043;
                                                                                                                                                                                                                                Evelopment 125:743-752(1998).

EMBL; V15837; CAA75799.1; --
HSSP; P49763; IR2N
GO: GO: 0016620; C: membrane; IEA.
GO; GO: 0008181; P: growth factor activity; IEA.
GO; GO: 0008181; P: growth and/or maintenance; IEA.
InterPro; IPR002400; GF_cysknot.
InterPro; IPR002400; GF_cysknot.
InterPro; IPR0024015; PO_growth_factor.
FFam; PF03128; CXCXC, FF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0016020; C:membrane; IEA.
GO; GO:0008083; F:growth factor activity; IEA.
GO; GO:00080151; P:cell growth and/or maintenance; IEA.
InterPro; IPR004153; CXCXC_repeat.
InterPro; IPR002400; GF_cysknot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence updat
01-UN-2003 (TrEMBLrel. 24, Last annotation upd
Vascular endothelial growth factor C precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0438; GECYSKNOT.
ProDom; PD001629; PD_growth_factor; 1.
SMART; SM00141; PDGF; 1.
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Coturnix coturnix (Common quail)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46839 MW;
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71.4%;
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                                                                                                      SEQUENCE FROM N.A.
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                                                                       NCBI_TaxID=9091;
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                                                    Coturnix
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SIGNAL
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Matches

09XS50

RESULT 6 Q9XS50

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G.Y.,

891 AA

PRT;

PRELIMINARY;

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Query Match
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Q918V8
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X MEDLINE=20530913; PubMed=11076861;
A Shibate K., Itch M., Azawa K., Nagaoka S., Sasaki N., Carninci P., A Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itch M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., A Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Izawa M., Ohara E., Watahiki M., A Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";

EMBL; AKO16632; BAB30348.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRANN=C57BL/6J; TISSUE=Testis;
STRANN=C57BL/6J; TISSUE=Testis;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Wonno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Franci P., Subbraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                    the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiracka T., Hoxi F., Imotani K., Ishii Y., Itoh M., Kasukawa T., Kato H., Kawai J., Kojima Y., Kojima Y., Kojima Y., Kojima Y., Kojima Y., Kojima Y., Kojima Y., Kojima Y., Kojima Y., Kojima Y., Kojima Y., Kojima Y., Owa C., Saito H., Numazaki R., Ohno M., Okazaki Y., Okido T., Owa C., Saito H., Saito H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tajima Y., Toya T., Yamamura T., Yamunishi A., Yoshida K., Yoshino M., Muramateu M., Hayashizaki Y., Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.0%; Score 50; DB 11; Length 888;
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888 AA; 95846 MW; E42D3971F1F95484 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=C57BH/6J; TISSUE=Testis;
MEDLINB=99279253; Pubmed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 3.9;
1; Mismatches
                                                                                                                                                                                                                   SEQUENCE FROM N.A. TISSUE-Testis; STRAIN-CSTRIG 67 MEDLINE-22354683; Pubmed=12466851; The FANTOM CONSORTIUM,
                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; PT0546; PT0698.
MGD; MGI:1921643; 4933403G14Rik.
Hypothetical protein.
NON TER. 888 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    RIKEN FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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SEQUENCE
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=C257BL/6J; TISSUE=Aorta, and Vein;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20330357; PubMed=10871370; Maizel J.V. Jr., Rybak S.M.; Chen S.-L., Le S.-Y. Newton D.L., Maizel J.V. Jr., Rybak S.M.; Apader-specific mRNA encoding a cytotoxic ribonuclease contains a structure. ; Transcal length and structure. ; Mucleic Acids Res. 28:2375-2382(2000). RNs., AF165133; AAP76935.1; -... RNR., A99035; A39035; A39035. Roucleic acid binding; IEA. GO:0003876; F:nucleic acid binding; IEA. GO:0004822; F:pancreatic ribonuclease activity; IEA. InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia; Batrachia; Anura; Neobatrachia, Ranoidea; Ranidae, Rana.
NCBI_TaxID=8404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.0%; Score 50; DB 11; Length 891; 64.3%; Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AK080043; BAC37814.1; -.
PIR; PT0546; PT0698.
PIR; PT0645; PT0645.
MGD; MG1:1921643; 4933403G14Rik.
Hypothetical protein.
SEQUENCE 891 AA; 96154 MW; 471D83C532E85A55 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14491 MW; B8511DC5407AB69B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Oncomase variant rapLR1 precursor.
Rana pipiens (Northern leopard frog).
                                       Last sequence update)
Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical serine-rich region containing protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 127 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.3%; Pred. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.0%; Score 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Probom; PD000535; RNaseA; 1.
SMART; SM00092; RNASe_PC; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
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260 TELDFETNTFCPPP 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 64.3
Matches 9; Conservative
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                                                                                                                           Mus musculus (Mouse)
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                                                                                                                                                                                 NCBI_TaxID=10090;
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Gaps

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Indels

Length 746;

us-09-761-636a-8.open.rspt

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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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MEDLINE-2260414; PubMed=12721629;
Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Ada regulatory protein/6-O-methylguanine-DNA methyltransferase.
ADAA OR BASS69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wilkinson J.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus anthracis (strain Ames).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=198094;
                EMBL; AX136403; AAM97069.1; -.
EMBL; BT000226; AAM15545.1; -.
HYpochetical protein.
SEQUENCE 746 AA; 82598 MW; D3E6FBB7C9161084 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003341; DUF139.
Pfam; PF02363; C_tripleX; B.
SEQUENCE 330 AA; 36605 MW; F043B1A90D3ABFE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                    DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.0%; Score 48; DB 5;
41.2%; Pred. No. 3.2;
ive 4; Mismatches (
                                                                                                                                                  Score 48.5; DE
Pred. No. 6;
3; Mismatches
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                                                                                                                                                                                                                                                 1 CASELGKSTNTF-----CKPPC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=99069613; Pubmed=9851916;
                                                                                                                                                  48.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z81129; CAB03405.1; -.
PIR; T25169; T25169.
                                                                                                                                               Query Match
Best Local Similarity 35.77
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WormPep; T23F1.6; CE14080.
InterPro; IPR003341; DUF12
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                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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018118
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Matches
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Q81WU7
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Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,
Deng J.M., Hayashizaki Y., Hsuan V.W., Lee J.M., Ishlda J., Kamiya A.,
Kawai J., Kim C.J., Narusaka M., Quach H.L., Sakurai T., Satou M.,
Seki M., Shinn P., Tang C.C., Toroumi M., Wallender B.K., Wong C.,
Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J.,
Theologis A., Davis R.W.,
Submitted (UUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                    01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
Genomic DNA, chromosome 5, BAC clone:F17P19.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Erassicales; Brassicaceae; Arabidopsis.
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Ecker J., Theologis A., Davis R.W.; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Η.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Structural analysis of Arabidopsis thaliana chromosome 5. XI."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10; Length 746;
                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                   3;
     69.2%; Pred. No. 0.79;
                                                                                                                                                                                                                                                                 746 AA
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                                   1; Mismatches
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583 CSEVMEKSTNSFSSAFDSTLADLCKDPC 610
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                                                                                                                                                                                                                                                                 PRT;
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98 CKYKLKKSTNTFC 110
                                                                              1 CASELGKSTNTFC 13
                             9; Conservative
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                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. Hypothetical protein.
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eurosids II; Bra
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                    Q9LTJ8;
01-OCT-2000
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01-OCT-2002
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                                                                                                                                                                                                   RESULT 11
Q9LTJ8
1D Q9LTJ8
DT 01-0C
DT 01-0C
DT 01-0C
DT 01-0C
DE Genom
OC Eukari
OC Eukari
OC Sperm
OC Sperm
OC STRAII
RN [1]
RN [1]
RR STRUK
RA TABAR
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Matches

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Retudat-Cairns J.R., Mizuno K., Fujimura T., Sriyotha P.;

Retudat-Cairns J.R., Mizuno K., Fujimura T., Sriyotha P.;

"Cloning, Expression, and Characterization of an Anti-fungal Chitinase Trem Leucaena leucocophala de Wit.";

Energian Jencechnol. Blochem. 0.0.0(2002).

Biosci. Biotechnol. Blochem. 0.0.0(2002).

Result, AFS13017; AAM49597.2; ...

RO; GO:0009507; C:chloroplast; IEA.

GO; GO:0009507; C:chloroplast; IEA.

RO; GO:0004568; F:chitin binding; IEA.

RO; GO:0006925; P:chitin catabolism; IEA.

RO; GO:0006032; P:chitin catabolism; IEA.

RO; GO:0006032; P:chitin binding_1:

BR Ffam; PR00187; Chitin bind_1: 1.

PR Ffam; PR00187; Chitin bind_1: 1.

PR Ffam; PR00187; CHITINBINDNG.

R ProDom; PD000609; CHITINBINDNG.

PRODOM; PD354900; Glyco_hydro_19; 1.
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   DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
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NCBI_TaxID=3866;
                                                                                                                                                                                                                    GO; GO:0005622; C:intracellular; IEA.
GO; GO:0008168; F:methyltransferase activity; IEA.
GO; GO:0003700; F:transfeription factor activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0008270; F:transferase activity; IEA.
GO; GO:0008281; P:DNA repair; IEA.
GO; GO:0006385; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR004026; Ada Zn bind.
InterPro; IPR000005; HTHATAG.
                                                                                                                       "The genome sequence of Bacillus anthracis Ames and comparison to closely related bacteria.";
Mature 423:81-86(2003).
EMBL; AE017036; AAP27604.1; -.
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Pred. No. 4.3;
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SMART; SM00342; HTHARAC.
SMART; SM00342; HTHARAC; 1.
PROSITE; PS01024; HTHARAC_FAMILY_1; 1.
PROSITE; PS01124; HTHARAC_FAMILY_2; 1.
Methyltransferase; Transferase; Complete proteome.
SEQUENCE 198 AA; 23280 MW; ABBECIA5A353170A CRC64;
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF02805; Ada Zn binding; 1. Pfam; PF00165; HTH AraC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.0%;
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01-CCT-2002 (TrEMBLrel. 22,
01-CCT-2003 (TrEMBLrel. 25,
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 KSTNTFCKPPC 17
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                                                                                                                   Fraser C.M.;
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DR PROSITE; PS00773; CHITINASE 19 1; 1.

DR PROSITE; PS00774; CHITINASE 19 2; 1.

DR PROSITE; PS00774; CHITINASE 19 2; 1.

RW Chitin-binding; Chloroplast.

SQ SEQUENCE 326 AA; 34908 MW; F73514268A84A46D CRC64;

Query Match

Best Local Similarity 47.4%; Pred: No. 7.2;

Matches 9; Conservative 2; Mismatches 6; Indels 2; Gaps

Qy 1 CASELG--KSTNTFCKPPC 17

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Db 41 CCSQFGWCGSTNDYCGPGC 59

Search completed: September 5, 2004, 09:59:58

Job time: 40.4646 secs
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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Scoring table:

1586107 seqs, 282547505 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:*
geneseqp2000s:*
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geneseqp2001s:*
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geneseqp2001s:* A_Geneseq_29Jan04:* geneseqp2003bs:* geneseqp2004s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Description	Aau04527 VEGE base	O VEGF bas	6 VEGF	7 VEGF	1 VEGF	Aau04549 VEGF base	Aau04548 VEGF base	2 Human		9 Human	1 Human	Human	Human	Human	O Homo	CI	3 Нишап	Aaw49036 Human zve	ന			Human	Himan 9	6 Human	Human
a.	AAU04527	AAU04550	AAU04546	AAU04547	AAU04551	AAU04549	AAU04548	AAU04522	AAU04520	AAY23889	AAB11931	ABB84621	ABG73750	ABG73779	AAW53240	AAY97572	AAW44293	AAW49036	AAW53241	AAB10649	AAY70750	AAY70983	AAB29049	AAB37606	AAB70685
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% Query Match	100.0	97.0	97.0	93.0	93.0	93.0	89.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	ö	0	ö	ö	٠	80.0	80.0	80.0
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-	Aau08441 Polypepti	Abg33055 Human vas	-	Abb84623 Human VEG	Human		Aam47933 Mouse VEG	Aay08287 Human gro		_			_	_	Aaw53242 Mus muscu	Aam47930 Mouse VEG	•	-	VEGF
AAY97573	AAU08441	5 ABG33055	5 ABG32046	5 ABB84623		2 AAW14994	5 AAM47933	AAY08287	. AAW53243	. AAM47931	AAW44296	AAY08286	. AAW14992	. AAW44295	AAW53242	. AAM47930	. AAU04524	. AAU04534	AAU04535
354 4	354 4	354 5		354 6			110 5	178 2	321 2	321 5	326 2	337 2	358 2	358 2	358 2	358 5	13 4	13 4	13 4
80.0	0.08	0.08	80.0	0.08	0.08	80.0	77.0	77.0	77.0	77.0	77.0	77.0	77.0	77.0	77.0	77.0	72.0	0.69	65.0
80	98	80	80	80	80	80	11	11	77	77	77	11	77	77	77	77	72	69	65
26	77	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

VEGF based bicyclic dimeric peptide #1. AAU04527 standard; protein; 17 AA. (first entry) 26-SEP-2001 AAU04527; AAU04527
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AC AAU0
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Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.

Synthetic.

/note= "A disulfide bond forms between residue 17 and residue 17 of an identical peptide to form a dimeric peptide, or to residue 1 of the sequence appearing as AAU04528, also forming a dimeric peptide" Location/Qualifiers 1. 13 /note= "This bond cyclises the peptide" 17 Key Disulfide-bond Disulfide-bond

WO200152875-A1

26-JUL-2001

18-JAN-2001; 2001WO-US001533.

18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P.

(LUDW-) LUDWIG INST CANCER RES

Cendron A; Ś Stacker Hughes RA, Achen MG,

WPI; 2001-442248/47.

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.

Claim 59; Page 32; 102pp; English.

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Locyclasation are used to interfere with any department of the condition characterised by angiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy.

The condition is diabetic retinopathy, psoriasis, arthropathy.

Cerebrovascular accident, post-angioplasty restencis, head, heat or cold traum, substance-induced medvascularisation of the liver, excessive trauma, substance-induced neovascular sequelae, or chronic liver sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability or nammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to inage blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF. Or -D and are also used in combination with an anti-inflammatory agent, to treat a
The sequence represents a dimeric bicyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptides from some peptides. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "A disulfide bond forms between residue 17 and residue 1 of the sequence appearing as AAU04528, forming a dimeric peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chronic inflammation, especially rheumatoid arthritis, psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .. .13 "This bond cyclises the peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 100; DB 4;
100.0%; Pred. No. 6.2e-08;
cive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VEGF based bicyclic dimeric peptide #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU04550 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CASELGKSINTFCKPPC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CASELGKSTNTFCKPPC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JAN-2000; 2000US-0176293P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JAN-2001; 2001WO-US001533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200152875-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU04550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
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Length 17; Indels

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The sequence represents a dimeric bicyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGEPD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-ce beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the peptide by oxidising the peptide by oxidising the cyclic peptides. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with anglogenesis.

CC peptides) and a cyclic peptide with at least one amino acid deleted prior co-cyclication are used to interfere with anglogenesis.

CC peptides and acyclic peptide with a condition characterised by anglogenesis, neovascularisation or lymphangiogenesis.

CC recondition is diabetic retinopathy, postiasis, arthropathy, cerebrovascular accident, post-angloplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive to remone-related anglogenic dysfunction, diabetes induced neovascular conficent accumulation in pertiples are also used to modulate vascular permeability in a committee. The monomeric and bicyclic peptides are used to image blood vessels and lymphatic contraction. The peptides are used to image blood vessels and lymphatic contraction in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic contraction in peripheral limbs or in lungs, peritoneal cavity, bleura, are also used in combination with an anti-inflammatory agent, to treat a continuation inflammatory agent, to treat a continuation inflammatory agent, to treat a continuation inflammatory and arthritis, psoriasis and
                                                                                                                        Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; VEGF; vascular endothelial growth factor; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neovascularisation, lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .13 /note= "This bond cyclises the peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97.0%; Score 97; DB 4; I
94.1%; Pred. No. 1.7e-07;
                                             Cendron A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEGF based bicyclic dimeric peptide #3.
                                                                                                                                                                                                                                          Example 26; Page 49; 102pp; English.
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                                           Stacker S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU04546 standard; peptide; 17
(LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CASELGKSTNTFCKPPC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CASELGKSTNTYCKPPC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 94.1
nes 16; Conservative
                                             Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diabetic retinopathy
                                                                                      WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disulfide-bond
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                                             Achen MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU04546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                   residues,
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Matches
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0
                                                                                                                                                                                                                                                                                                              or cold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to treat a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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The sequence represents a dimeric bicyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human versely (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betactor beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide with at least one amino acid deleted prior of cyclisation are used to interfere with anglogenesis, convexicularisation or lymphangiogenesis, neovascularisation or lymphangiogenesis, neovascularisation or lymphangiogenesis, chearacterised by angiogenesis, neovascularisation or lymphangiogenesis.

The condition is diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-aminoplasty restenosis, head, heat or cold carebrovascular accident, post-aminoplasty restenosis, head, heat or crebrovascular accident, post-aminoplasty restenosis, head, heat or crebrovascular accident, post-aminoplasty restenosis, head, heat or cold hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere care used to interfere care also used in combination with an anti-inflammatory agent, to treat a care incertional inflammatory agent, to treat a care incertional partition with an anti-inflammatory pager, yespecially reteriors in the peptides are also u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 26; Page 49; 102pp; English.
                                                                                                                                                                                                                                                                                                                       (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                               18-JAN-2001; 2001WO-US001533.
                                                                                                                                                                                                                                              18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                                                                                                                                        Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-442248/47
                                                                                               WO200152875-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17 AA;
                                                                                                                                              26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                        Achen MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      residues.
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Cendron A;

Example 26; Page 49; 102pp; English

residues

Gaps 0 97.0%; Score 97; DB 4; Length 17; 94.1%; Pred. No. 1.7e-07; Live 1; Mismatches 0; Indels 1 CASELGKSINTFCKPPC 17 Conservative Local Similarity 16; Query Match Matches à

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CATELGKSTNTFCKPPC

AAU04547 standard; peptide; 17 AA. AAU04547; RESULT 4
AAU04547
ID AAU0
XX
AC AAU0
XX
DT 26-S

(first entry) 26-SEP-2001

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine /note= "A disulfide bond forms between residue 17 and residue 17 of an identical peptide to form a dimeric Human, VEGF, vascular endothelial growth factor; angiogenesis neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; 1. .13
/note= "This bond cyclises the peptide" diabetic retinopathy; chronic inflammation; cyclic. VEGF based bicyclic dimeric peptide #4. Location/Qualifiers Stacker S, (LUDW-) LUDWIG INST CANCER RES. 18-JAN-2001; 2001WO-US001533. 18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P. peptide" Achen MG, Hughes RA, WPI; 2001-442248/47. Disulfide-bond Disulfide-bond WO200152875-A1 26-JUL-2001 Synthetic Novel Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine /note= "A disulfide bond forms between residue 17 and residue 17 of an identical peptide to form a dimeric Cendron A; Stacker S,

The Sequence represents a commenter Director of the invention, whose 3 dimensional structure is modelled on the expose loop of human UNGED (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabeta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptides by oxidising the periode of growth factor protein and cyclising the peptide by oxidising the periode comprising 2 linked monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis.

Co cyclisation are used to interfere with angiogenesis.

Co continuous acided to interfere with angiogenesis.

Characterised by angiogenesis, neovascularisation or lymphangiogenesis.

Che condition is diabetic retinopathy, psoriasis, arthropathy, chemangioma, vascularised malignant or benjan tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold traums, substance-induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and cheromic inflammation with an anti-inflammatory agent, to treat a chronic inflammation in peripherally with an enti-inflammatory agent, to treat a chronic inflammation in peripherally with an enti-inflammatory agent, to treat a chronic inflammation in peripherally with an enti-inflammatory agent, to treat a chronic inflammation inflammation with an enti-inflammatory accumulation with an enti-infl sequence represents a dimeric bicyclic peptide of the invention, inflammation, especially rheumatoid arthritis, psoriasis

Gaps .; 0 Score 93; DB 4; Length 17; Pred. No. 6.9e-07; 2; Mismatches 0; Indels 2; Mismatches 93.0%; 88.2%; 15; Conservative Best Local Similarity Query Match Matches

diabetic retinopathy

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The sequence represents a dimeric bicyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human CV WighPD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betaction exparation distances on opposite antiparallel strands of a petide loop fragment from an exposed loop of a growth factor protein and cyclic peptide by oxidising the cycleine residues. The monocyclic peptides, dimeric bicyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, covascularisation or lymphangiogenesis in a mammal with a condition of cyclisation is diabetic retinopathy, psoriasis, arthropathy, cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive correction. The oppliedes are also used to modulate vascular permeability in fection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "A disulfide bond forms between residue 17 and residue 1 of the sequence appearing as AAU04528, forming a dimeric peptide"
                                                                                                                                                                                                                                                                        Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                            l. .13
/note= "This bond cyclises the peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cendron A;
                                                                                                                                                                                                                                       VEGF based bicyclic dimeric peptide #8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 26; Page 49; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stacker S,
                                                                                                                               AAU04551 standard; peptide; 17 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LUDW-) LUDWIG INST CANCER RES
                   CASELGKTSNTFCKPPC 17
CASELGKSTNTFCKPPC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JAN-2000; 2000US-0176293P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-JAN-2001; 2001WO-US001533.
                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                                                                                                                                                        Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disulfide-bond
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                                                                                                                                                                                                      26-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Achen MG,
                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                 AAU04551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         residues.
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The sequence represents a dimeric bicyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human NGEDD (vascular endothellal growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabeta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
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O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF. VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "A disulfide bond forms between residue 17 and residue 17 of an identical peptide to form a dimeric
                                                                                                                                                                                        Gaps
                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                       93.0%; Score 93; DB 4; Length 17; 88.2%; Pred. No. 6.9e-07; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . .13 note= "This bond cyclises the peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cendron A;
                                                                                                                                                                                                                                                                                                                                                                                                                                           VEGF based bicyclic dimeric peptide #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 26; Page 49; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stacker S,
                                                                                                                                                                                                                                                                                                                                           AAU04549 standard; peptide; 17 AA
                                                                                                                                                                                     2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                          1 CASELGKSTNTFCKPPC 17
                                                                                                                                                                                                                                                         17
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                                                                                                                                                                                                                                           CASELGRSTNSFCKPPC
                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                          15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                                                                                                                                             (first
                                                                                                                                                                           Similarity
                                                                                                                        Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                             26-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                            AAU04549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      residues.
                                                                                                                                                         Query Match
                                                                                                                                                                            Best Local
                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                             RESULT 6
                                                                                                                                                                                                                                                                                                                           AAU04549
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to cyclisation are used to interfer with angiogenesis,

neovascularisation or lymphangiogenesis in a mammal with a condition
characterised by angiogenesis, neovascularisation or lymphangiogenesis.

The condition is diabetic retinopathy, psoriasis, archropathy,
bemangioma, vascularised malignant or benign tumour, post-recovery
cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
trauma, substance-induced neovascularisation of the liver, excessive
hormone-related angiogenic dysfunction, diabetes induced neovascular
confection. The peptides are also used to modulate vascular permeability
in a mammal (the mammal has a condition characterised by fluid
communation in peripheral limbs or in lungs, peritoneal cavity, pleura,
or brain. The peptides are used to image blood vessels and lymphatic
vasculature. The monomeric and bicyclic peptides are used to interfere
are also used in combination with an anti-inflammatory agent, to treat a
chronic inflammation, especially rheumatoid archritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                 ò
peptides) and a cyclic peptide with at least one amino acid deleted prior
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "A disulfide bond forms between residue 17 and residue 17 of an identical peptide to form a dimeric
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; VEGF; vascular endothelial growth factor; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neovascularisation, lymphangiogenesis, psoriasis, tumour;
diabetes induced neovascular sequelae, rheumatoid arthritis,
diabetic retinopathy, chronic inflammation, cyclic.
                                                                                                                                                                                                                                                                                                                                                            93.0%; Score 93; DB 4; Length 17; 88.2%; Pred. No. 6.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                              0; Indels

    .13
/note= "This bond cyclises the peptide"

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                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VEGF based bicyclic dimeric peptide #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU04548 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stacker S,
                                                                                                                                                                                                                                                                                                                                                                                            ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CASELGRSTNSFCKPPC 17
                                                                                                                                                                                                                                                                                                                                                                                                                            CASELGKSINTFCKPPC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-JAN-2000; 2000US-0176293P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JAN-2001; 2001WO-US001533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 88.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                                                            Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200152875-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU04548;
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The sequence represents a dimeric bicyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human CV WEGPD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis.

CC peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis.

CC peptides and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis.

CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.

CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.

CC crebrovascular accident, post-angioplasty restenosis, head, heat or claumer condition is diabeted resident to be benign tumour, post-recovery created angiogenic dysfunction, diabetes induced neovascular created angiogenic dysfunction, diabetes induced neovascular created accumulation in pertipheral limbs or in lungs, peritoned accumulation in pertipheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere covery cor brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere covery cor brain combination with an anti-inflammatory agent, to treat a corporation in perinonary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
  from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VEGF-D; vascular endothelial growth factor; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neovascularisation, lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 89; DB 4; Length 17;
Pred. No. 2.7e-06;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cendron A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human VEGF-D amino acids Val101-Thr 173.
                                                                  Example 26; Page 49; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU04522 standard; protein; 73 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (LUDW-) LUDWIG INST CANCER RES
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16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 80.68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CASELGKSTNTFCKPPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CASDVGKSTNTWCKPPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 82.4
Matches 14, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200152875-A1.
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                    residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU04522;
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or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine Novel monomeric monocyclic peptide, used to interfere with anglogenesis, WPI; 2001-442248/47 residues 

The sequence represents Human VEGF-D (vascular endothelial growth factor)

amino acids Val101-Thr 173, used together with the C-terminal 23 residues

of VEGF to make a hybrid theoretical molecule for 3 dimensional

modelling. The sequence is used in a method of producing a monomeric

monocyclic peptide by a measuring beta-beta carbon separation distances

con opposite antiparallel strands of a peptide loop fragment from an

exposed loop of a growth factor protein and cyclising the peptide by

cxidising the cysteine residues. The monocyclic peptides dimeric

betyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic

cyclic peptide with at least one amino acid deleted prior to cyclisation are

used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition of a racterised by

angiogenesis, neovascularisation or lymphangiogenesis. The condition is

diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised

conditional paths are sequelae, neovascular sequelae, hypertension induced

neovascularisation of the liver, excessive hormone-related angiogenic

dysfunction, diabetes induced neovascular sequelae, hypertension induced

neovascular sequelae, or chronic liver infection. The peptides are also

used to modulate vascular permeability in a mammal (the mammal has a

condition characterised by filled accumulation in peripheral limbs or in

condition characterised by filled accumulation in peripheral. lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy Example 1; Page 90-91; 102pp; English Sequence 73 AA;

Gaps .; 0 80.0%; Score 80; DB 4; Length 73; 93.8%; Pred. No. 0.00024; 1; Indels 0; Mismatches 15; Conservative Query Match Best Local Similarity Matches

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AAU04520 standard; protein; 96 AA. RESULT 9 AAU04520

AAU04520;

26-SEP-2001 (first entry)

Human VEGF-D amino acide Val101-PRO186.

Human; VEGF-D; vascular endothelial growth factor; anglogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation.

Home sapiens

WO200152875-A1.

26-JUL-2001.

18-JAN-2001; 2001WO-US001533 

18-JAN-2000; 2000US-0176293P.

16-MAY-2000; 2000US-0204590P.

(LUDW-) LUDWIG INST CANCER RES

Cendron A; Stacker S, Hughes RA, Achen MG,

WPI; 2001-442248/47.

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine

Example 1; Page 89; 102pp; English.

The sequence represents running vorces (vascular announces) and acids valid-pRQ186. The sequence is used in a method of producing a monomeric monocyclic peptide by a measuring beta-beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptides. Ownerising 2 linked monocyclic peptides, dimeric by oxidising the cysteine residues. The monocyclic peptides dimeric peptides (omprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, archropathy, hemangioma, vascularised najioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, hypertension induced neovascular sequelae, hypertension induced neovascular sequelae, hypertension induced neovascular sequelae, hypertension induced neovascular sequelae, hypertension induced neovascular sequelae, hypertension induced neovascular sequelae, hypertension induced neovascular sequelae, hypertension induced neovascular sequelae, hypertension induced neovascular sequelae, hypertension induced neovascular sequelae, hypertension induced neovascular sequelae, hypertension induced neovascular sequelae, hypertension induced neovascular sequelae, neovascular sequelae, neovascular sequelae, hypertension induced neovascular sequelae, hypertension induced neovascular sequelae, hypertension induced neovascular sequelae, neovascular sequelae, neovascular sequelae, neovascular sequelae, neovascular sequelae, neovascular sequelae, neovascular sequelae, neovascular sequelae, neovascular sequelae, neovascular sequelae, neovascular sequ condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic The sequence represents Human VEGF-D (vascular endothelial growth factor) peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy

Sequence 96 AA;

.. 0

Gaps .. 80.0%; Score 80; DB 4; Length 96; 93.8%; Pred. No. 0.00031; Live 0; Mismatches 1; Indels 93.8%; Pic. Local Similarity 93.6 Query Match Matches

. 0

17 21 ASELGKSTNTFFKPPC 36 2 ASELGKSTNTFCKPPC à g

RESULT 10

AAY23889

AAY23889;

AAY23889 standard; protein; 109 AA.

(first entry) 21-SEP-1999 Human vascular endothelial growth factor (VEGF)-D.

Vascular endothelial growth factor; VEGF; VEGF-D; malignant melanoma; tumour; psoriasis; angiogenesis; lymphangiogenesis; skin graft; wound healing; lymphedema; scleroderma; anhydrotic ectodermal dysplasia.

Homo sapiens

WO9933485-A1

08-JUL-1999. 

98WO-US027373. 23-DEC-1998;

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RESULT 12
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                                                                                                                                                                         The present sequence represents human vascular endothelial growth factor (VEGF)-D. The specification describes a human cell line which stably expresses VEGF-D, or fragments/analogues having VEGF-D biological activity. VEGF-D antagonists, e.g. antisense nucleic acids or triplex activity. VEGF-D antagonists, e.g. antisense nucleic acids or triplex DNA, VEGF-D variants or antibodies (especially chimeric antibodies), are useful for the treatment or alleviation of malignant melanomas, tumours or psoriasis. Angiogenesis and lymphagiogenesis stimulating amounts of vEGF-D can be administered to enhance the acceptance and/or healing of skin grafts or to stimulate the healing of a surgical or traumatic wound to the skin. Lymphagiogenesis stimulating amounts of vEGF-D can be used to treat scheroderma. Vascularisation stimulating amounts of vEGF-D are used to treat anhydrotic ectodermal dysplasia. VEGF-D antibodies are useful for detecting tumours expressing vEGF-D. Fully.

The consense of vEGF-D can be used to stimulate at least one VEGF-D bloactivity chosen from endothelial cell proliferation, migration, survival and differentiation and lymphangiogenesis without inducing vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                          growth factor D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Truncated VEGF-D; vascular endothelial growth factor; human;
monoclonal antibody; VEGF receptor; VEGFR-2; VEGFR-3;
vascular permeability disorder; endothelial cell proliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   angiogenic disorder; lymphangiogenic disorder; professioner meovascularisation disorder; endothelial cell differentiation disorder; cancer; diabetic retinopathy; psoriasis; arthropathy; pulmonary oedema; detection; diagnosis; imaging; lymphatic vasculature.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               .,
                                                                                                                                                                                                                                                                                                                                                                                                                                   80.0%; Score 80; DB 2; Length 109; 93.8%; Pred. No. 0.00036; ive 0; Mismatches 1; Indels
                                                                                                                    A human cell line stably expressing vascular endothelial cuseful for treating melanomas or tumors expressing {
m VEGF-D}_{-}^{-}
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                        Alitalo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB11931 standard; protein; 109 AA.
                                                                                                                                                     Claim 6; Page 72; 79pp; English
                                              (LUDW-) LUDWIG INST CANCER RES
            97AU-00001131.
98US-0087392P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17
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99US-0134556P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 ASELGKSTNTFFKPPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 ASELGKSTNTFCKPPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                       Stacker SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human truncated VEGF-D.
                                                                                             WPI; 1999-405368/34.
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 109 AA;
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            24-DEC-1997;
29-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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17-MAY-1999;
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                                                                       Achen MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB11931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
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(Vascular endothelial growth factor D), lacking both the N- and C-terminal regions. The invention relates to a monoclonal antibody, or fragments thereof, which is specifically reactive with the truncated human VEGF-D, and methods of preparing the antibody. The antibody of the invention interferes with the binding of VEGF-D to the VEGF receptors. VEGFR-2 and VEGFR-3, but does not interfere with the binding of VEGF to these receptors and additionally is not reactive with VEGF-C. The antibody may be used to treat disorders associated with vascular permeability, endothelial cell proliferation, angiogenesis, lymphangiogenesis, neovascularisation and endothelial cell. Wifferentiation, especially cancer, diabetic retinopathy, psoriasis, and arthropathies. The antibody may also be used to treat fluid accumulation in the heart and/or lung via modulation of vascular permeability. It may additionally be used to detect VEGF-D and may be used to image lymphatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        o,
                                                                                                                                                                                                     Novel compositions comprising antibodies reactive to vascular endothelial growth factor-D, useful for treating, e.g. angiogenesis, lymphogiogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, single-chain, extracellular ligand-binding domain, VEGF, vascular endothelial growth factor, VEGF type 2 receptor, KDR; Flt-4; VEGF type 3 receptor; VEGF-C; VEGF-D; signal transduction, angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "region of monomer likely to be modified by mutation as described in claim 9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                monomer likely to be modified by lbed in claim 9"
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                                                                                                                                                                                                                                                                                                                                                                                                       sequence represents a 109 amino acid truncated human VEGF-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.0%; Score 80; DB 3; Length 109; 93.8%; Pred. No. 0.00036; rive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55. .60
/note= "region of monomer likel
mutation as described in claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human wild-type VEGF-D monomer SEQ ID 3.
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                                                                                                                                                                                                                                                                        and neovascularization disorders.
(LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 1; 44pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .86
                                                               Achen MG, Stacker SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vasculature in tissue
                                                                                                                                         WPI; 2000-442498/38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lymphangiogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 109 AA;
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This invention describes a novel single-chain dimeric polypeptide which binds to extracellular ligand-binding domain of vascular endothelial growth factor (VEGF) type 2 receptor (RDR) or VEGF type 3 receptor (FIL-G). The polypeptide of the invention comprises two receptor-binding sites of which one is capable of binding to a ligand-binding domain of the receptor, and at least one monomer of the dimeric domain of the receptor, and at least one monomer of the dimeric polypeptide is derived from VEGF. VEGF-C or VEGF-D, where the polypeptide is capable of binding to the receptor, but incapable of activating the receptor. The polypeptide of the invention is useful for preparing a medicament for preventing or treating a disease or condition involving increased signal transduction from, or an increased activation of a VEGF-D increased signal transduction from, or an increased activation of a VEGF-D invented in the construction of a VEGF-D monomer which can be modified and used in the construction of a VEGF-D monomer which can be modified in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "This wild-type residue is replaced by Arg or Glu in the first monomer unit of the VEGF-D dimer if the E57R mutation has not occurred (see Claim 16) and is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; single-chain; extracellular ligand-binding domain; VEGF;
vascular endothelial growth factor; VEGF type 2 receptor; KDR; Flt-4;
VEGF type 3 receptor; VEGF-C; VEGF-D; signal transduction; angiogenesis;
                                                                                                                                                                                                                                                                                                   Novel single-chain dimeric polypeptide for inhibiting angiogenesis, bit to extracellular ligand-binding domain of vascular endothelial growth factor type 2/type 3 receptor but does not activate the receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80.0%; Score 80; DB 6; Length 109; 93.8%; Pred. No. 0.00036; ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                 Claim 9; Page 66; 71pp; English.
                                                                                                                                 06-APR-2001; 2001DK-00000578.
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                                                                                             08-APR-2002; 2002WO-DK000233.
                                                                                                                                                                                         (MAXY-) MAXYGEN HOLDINGS LTD.
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                                                                                                                                                                                                                                                                 WPI; 2003-058505/05.
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Misc-difference
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                   WO200281520-A2.
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                                                       17-0CT-2002
                                                                                                                                                                                                                               Boesen TP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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/note= "This wild type Phe residue is optionally replaced by Arg in the second monomer unit of the VEGF-D dimer (see Claim 11)"
                                                                                                                                                                                                                                                                                                          /note= "This wild type lle residue is optionally replaced by Arg or Glu in the second monomer unit of the VEGF-D dimer (see Claim 16)"
                                                                                                /note= "This wild type Thr residue is optionally replaced by Arg or Glu in the second monomer unit of the VEGF-D dimer (see Claims 11 and 16)"
                                                                                                                                             /note= "This wild type Phe residue is optionally replaced by Arg or Glu in the second monomer unit of the VEGF-D dimer (see Claims 11 and 16)"
                                                  /note= "This wild-type Asn residue is optionally replaced
by Arg in the second monomer unit of the VEGF-D dimer
(See Claim 11)"
                                                                                                                                                                                                                                        /label= E57R
/note= "Wild type Gln is replaced by Arg in the first
monomer unit of the VEGF-D dimer (See Claim 11) and is
optionally replaced if the S10R/E mutation has occurred
(see Claim 16)"
optionally replaced if the E57R mutation has occurred. The claim describes this residue as Ser but is shown as Ile in the sequence listing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MAXY-) MAXYGEN HOLDINGS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                06-APR-2001; 2001DK-00000578
                                                                                                                                                                                                                                                                                                                                                                                                                                           06-APR-2001; 2001US-0282239P
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                                                                                                                                                                                  Misc-difference 40
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                                          Misc-difference 37
                                                                                         Misc-difference 38
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binds

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Gaps ; 0 Novel single-chain dimeric polypeptide for inhibiting angiogenesis, binds to extracellular ligand-binding domain of vascular endothelial growth factor type 2/type 3 receptor but does not activate the receptor.

Claim 11; Page; 71pp; English.

This invention describes a novel single-chain dimeric polypeptide which binds to extracellular ligand-binding domain of vascular endothelial commoder to the polypeptide of the invention comprises two receptor (PIT-C 4). The polypeptide of the invention comprises two receptor-binding sites of which one is capable of binding to a ligand-binding domain of the receptor, and at least one monomer of the dimeric domain of the receptor, and at least one monomer of the dimeric collapseptide is derived from VEGF. VEGF-C or VEGF-D, where the polypeptide of the invention is useful for preparing a receptor. The polypeptide of the invention is useful for preparing a receptor. The polypeptide of the invention is useful for preparing a medicament for preventing or treating a disease or condition involving increased signal transduction from, or an increased activation of a VEGF or type 2 or type 3 receptor e.g. for inhibiting angiogenesis or type 3 receptor e.g. for inhibiting angiogenesis or type 2 receptor e.g. for inhibiting angiogenesis or type 2 receptor e.g. for inhibiting angiogenesis or type 2 receptor e.g. for inhibiting angiogenesis or type 2 receptor e.g. for inhibiting angiogenesis or type 2 receptor e.g. for inhibiting angiogenesis or disclosure of the invention. In one instance a polypeptide is claimed comparising a first monomer derived from the apolypeptide is claimed comprising at least one mutation selected from the group consisting of N37R, T38T, F39R and F40R. In a second instance a polypeptide is claimed comprising a first monomer containing a substitution consisting of S10R, S10R and E57R (although the residue at position 10 is an Ile), and/or in

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the other VEGF-D derived monomer at least one substitution selected from the group consisting of T13R, T13R, F19R, F19E, I76R and I76E. NOTE: This sequence is not represented in the body of the specification but has been constructed from the wild-type VEGF-D sequence represented in ABB84621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New endothelial growth factor polypeptide and polynucleotides, useful for diagnosing, preventing, and treating cancer and other conditions or diseases involving angiogenesis and cell proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Encoded by TAA, an in frame stop codon which interrupts the coding region as shown in Figure 1A.B. This site is the end of the protein sequence represented in SEQ ID 1 of the Sequence listing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel human endothelial growth factor polypeptide which has cytostatic activity. The polypeptide and its encoding polymucleotide are useful in the diagnosis, prevention, and treatment of cancer and other conditions or diseases involving angiogenesis and cell proliferation. NVR may also be used to promote revascularisation following traumatic amputation and surgical reconstruction or added to a tissue culture to promote vasculogenesis in tissues for autologous or heterologous transplant. Antagonists or inhibitors of NVR may be used to suppress or prevent angiogenesis and
                                                                                                                                                                                                                                                                                                                                                                                                                          NVR; human; endothelial growth factor; cytostatic; cancer; angiogenesis; cell proliferation; revascularisation; amputation; vasculogenesis; transplant; brain; breast; intestine; kidney; lung; ovary; pancreas; prostate; uterus; gene therapy.
                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Region not represented in SEQ ID 1 of the
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                                                                                                                80.0%; Score 80; DB 6; Length 109; 93.8%; Pred. No. 0.00036; ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                             ABG73779 standard; protein; 287 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 1A-B; 28pp; English
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                                                                                                                                                                                                                                                                                                                                                                 entry)
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                                                                                             Query Match
Best Local Similarity
Local 15; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                            Human NVR protein.
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                                                                                 Sequence 109
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                                                                                                                                                                                                                                                                                                                             ABG73779;
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thus prevent the growth and development of cancers such as cancer of the brain, breast, intestine, kidney, lung, ovary, pancreas, prostate or uterus. The products of the invention can be used for gene therapy. This sequence represents the human NVR protein described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                          vascular endothelial growth factor; VEGF-D; angiogenesis; modification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated vascular endothelial growth factor-D - used to develop products for use in e.g. modifying angiogenesis or treating lung, heart or intestinal disorders.
                                                                                                                                                                                                                                                                                                                                                     acceleration, wound healing, tissue; organ; transplants; collateral circulation; infarction; arterial stenosis; coronary artery disease; inhibition; cancer; treatment; diabetic retinopathy; lung disorders, blood circulation; gaseous exchange; chronic obstructive airway disease; intestinal malabsorptive syndrome; blopsy; metastatic risk; detection; diagnosis; congestive heart failure.
                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156. 158 // Note= "potential N-linked glycosylation site" 258. 260 // Note= "potential N-linked glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "potential N-linked glycosylation site"
                                                                                                                                                                                                                                                                                                                  Homo sapiens vascular endothelial growth factor D (VEGF-D).
                                                                                         ; DB 6; Leus.
                                                                                                    Length 287;
                                                                                                  Score 80; DB 6
Pred. No. 0.000
0; Mismatches
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                                                                                                  80.0%;
93.8%;
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97AU-00004954.
97US-0038814P.
97AU-00007435.
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                                                                                                                                                   2 ASELGKSTNTFCKPPC
                                                                                                                                                                                                                                                                                        03-AUG-1998 (first entry)
                                                                                              Query Match
Best Local Similarity 93.8
Matches 15; Conservative
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                                                                           Sequence 287 AA;
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11-NOV-1996;
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Claim 16; Page 57-58; 101pp; English.

The sequence is that of human breast vascular endothelial growth factor D (VEGP-D). VEGP-D can be used for e.g. acceleration of angiogenesis in wound healing, tissue or organ transplantation, or to establish collateral circulation in tissue infarction or arterial stenosis, such as coronary artery disease, and inhibition of angiogenesis in the treatment of coronary artery disease, not inhibition of angiogenesis in the treatment of tung disorders to improve blood circulation in the lung and/or gascous exchange between the lungs and the blood stream or to improve blood circulation in the lungs and the blood stream or to improve blood circulation in the lungs of cardiac insufficiency, to improve blood flow and gascous exchange in che intestinal tract. Quantitation of VEGF-D in cancer blopsy in the intestinal tract. Quantitation of VEGF-D in cancer blopsy specimens may be useful as an indicator of future metastatic risk.

Changonists can be used for treating e.g. conditions such as congestive heart failure, involving accumulations of fluid in the lung resulting from increases in vascular permeability. The products can also be used confered to detection and diagnosis 

Sequence 325 AA;

Gaps . 0 80.0%; Score 80; DB 2; Length 325; 93.8%; Pred. No. 0.001; tive 0; Mismatches 1; Indels Query Match Best Local Similarity 93.84 Matches 15; Conservative

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2 ASELGKSTNTFCKPPC 17

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92 ASELGKSTNTFFKPPC 107

Search completed: September 5, 2004, 09:55:11 Job time : 55.8081 secs

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5 ; Search time 47.7374 Seconds (without alignments) 112.199 Million cell updates/sec
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1. (ggn2_6/ptodata/2/pubpaa/US06_MEW_PUB.pep:*
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1. (ggn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
1. (ggn2_6/ptodata/2/pubpaa/US08_MEW_PUB.pep:*
1. (ggn2_6/ptodata/2/pubpaa/US08_MEW_PUB.pep:*
1. (ggn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
1. (ggn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                              September 5, 2004, 10:00:15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1 CASELGKSTNTFCKPPC 17
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 8. Appli	27	Segmence 31 Appl	Sequence 28 Appl	Sequence 30. Appl	Semience 32 Appl	Semilaria of annumber	, ,	Semience 1. Appli	` `~	· · -	· _	·α	· -	Sequence 3, Appli
SUMMARIES		US-09-761-636A-8	US-09-761-636A-27	US-09-761-636A-31	US-09-761-636A-28	US-09-761-636A-30	US-09-761-636A-32	US-09-761-636A-29	US-09-761-636A-3	US-09-761-636A-1	US-09-956-095-3	US-09-219-345A-1	US-10-779-731-1	US-10-352-153-8	US-10-044-622-1	US-10-274-953-3
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% Query Match		100.0	97.0	97.0	93.0	93.0	93.0	89.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0
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US-10-161-694-3	US-09-956-095-2	US-09-219-345A-11	US-09-795-006A-119	US-09-375-248-6		_	US-10	US-10-274-953-5	US-10	US-10-174-930-1	US-10-139-876-4	US-10-139-876-5	US-10-086-623-18	US-10-260-539-18	US-09-847-524-6		US-10-274-953-9	US-10-161-	US-09-852-209A-13	US-09-847-524-2	US-10-439-337A-13	US-10-303-997B-13	US-10-139-876-2	US-10-131-600-13	US-10-274-953-8	US-10-161-694-8	US-09-761-636A-5	US-09-761-636A-15	US-09-761-636A-16
14	σ	σ	σ	10	12	12	14	14	14	14	13	13	13	14	10	10	14	14	σ	10	12	12	13	14	14	14	σ	0	σ
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80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	77.0	77.0	77.0	77.0	77.0	77.0	77.0	77.0	77.0	77.0	77.0	77.0	77.0	77.0	77.0	72.0	0.69	65.0
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16	17	18	19	20	21	22	23	24	25	26	27	28	53	30	31	32	33	34	35	36	37			40	41	42	43	44	45

### ALIGNMENTS

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US-09-761-636A-8

Sequence 8, Application US/09761636A

Sequence 8, Application US/09761636A

Sequence 8, Application US/09761636A

GENERAL INFORMATION:

APPLICANT: ACHEN, Marchard

APPLICANT: ACHEN, Angela

TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR

TITLE OF INVENTION: VEGF-0/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR

TITLE OF FILING DATE: 2000-01-18

PRIOR FILING DATE: 2000-01-18

PRIOR FILING DATE: 2000-01-18

PRIOR FILING DATE: 2000-0516

NUMBER OF SEQ ID NOS: 34

SEQ ID NO 8

SEQ ID NO 8

LENGTH: 17

TYPE: PRT

ORGANISM: Homo sapiens

US-09-761-636A-8

Query Match

Best Local Similarity 100.0%; Score 100; DB 9; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.2e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps
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Db 1 CASELGKSTNTFCKPPC 17

RESULT 2
US-09-761-636A-27

; Sequence 27, Application US/09761636A

; Patent No. US20020065518A1

0

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Gaps

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GENERAL INCURRANT.

GENERAL INCURRANT.

APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: CRUNCAN.

APPLICANT: CRUNCAN.

TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REPERENCE: 1064/48505 Achen et al
CURRENT FILING DATE: 2000-01-18
PRIOR PILING DATE: 2000-01-18
PRIOR PILING DATE: 2000-01-16
PRIOR PILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 30
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 32, Application US/09761636A
Patent No. US20020065218A1
Patent No. US20020065218A1
Patent No. US20020065218A1
APPLICANT: ACHEN, Marc
APPLICANT: GENDEN, Marc
APPLICANT: CENDENON, ABCF-C/VEGF PEPTIDOMIMETIC INHIBITOR
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT PEPLING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US/09/761,636A
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.0%; Score 93; DB 9; Length 17; 88.2%; Pred; No. 3.7e-07; . Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                               Length 17;
                                                                                                                                                                                                                                                                                                                                                                                               93.0%; Score 93; DB 9; Length 17;
88.2%; Pred. No. 3.7e-07;
ive 2; Mismatches 0; Indels
                    FILE REFERENCE: 1064/48505 Achen et al CURRENT APPLICATION NUMBER: US/09/761,636A CURRENT FILING DATE: 2001-01-18 PRIOR APPLICATION NUMBER: US 60/176,293 PRIOR FILING DATE: 2000-01-18 PRIOR FILING DATE: 2000-01-16 NUMBER OF SEQ ID NOS: 34 SOFTWARE: Patentin version 3.0 SOFTWARE: Patentin version 3.0 LENGTH: 17
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'Sequence 30, Application US/09761636A

; Septent No. US20020065218A1

; GENERAL INFORMATION:
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; ORGANISM: synthetic construct
US-09-761-636A-30
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US-09-761-636A-28
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Matches 15; Conservative
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Best Local Similarity
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US-09-761-636A-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:

APPLICANT: ACHEN, Marc
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: TYANER, Steven

APPLICANT: STACKER, Steven

TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
TITLE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A

CURRENT FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR PLILNG DATE: 2000-01-18
PRIOR PLILNG DATE: 2000-01-18
PRIOR PLILNG DATE: 2000-01-18
PRIOR PLILNG DATE: 2000-01-18
PRIOR PLILNG DATE: 2000-01-18
NUMBER OF SEQ 1D NOS: 34

NUMBER OF SEQ 1D NOS: 34

NUMBER OF SEQ 1D NOS: 34
                                 APPLICANT: ACHEN, Marc
APPLICANT: STACKER, Steven
APPLICANT: HUGHES, Nichard
APPLICANT: HUGHES, Nichard
APPLICANT: HUGHES, Angela
TITLE OF INVENITION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/4855 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT FILING DATE: 2001-01-18
PRIOR PLILIGATION NUMBER: US 60/176,293
PRIOR PLILIGATION NUMBER: US 60/204,590
PRIOR PLILIG DATE: 2000-01-18
PRIOR PLILIG DATE: 2000-01-18
NUMBER OF SED ID NOS: 34
SOFTWARE: Patentin version 3.0
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97.0%; Score 97; DB 9; Length 17;
Best Local Similarity 94.1%; Pred. No. 9.2e-08;
Matches 16; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 97; DB 9; Length 17; Pred. No. 9.2e-08; 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 31, Application US/09761636A Patent No. US20020065218A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CASELGKSTNTFCKPPC 17
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Best Local Similarity 94.1%;
Matches 16; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) ORGANISM: synthetic construct US-09-761-636A-27
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APPLICANT: STACKER, Steven
APPLICANT: HUGHES, Richard
APPLICANT: CENDRON, Angela
               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
US-09-761-636A-28
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US-09-761-636A-31
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Best Local Similarity
Matches 15; Conserv
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US-09-761-636A-1
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LENGTH: 96
         SEQ ID NO 3
LENGTH: 73
                                                                                                                                                                                                         Query Match
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; Patent No. US20020065218A1
; GENERAL INPORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: CENDRON, Angela
; APPLICANT: HUGHES, Richard
; APPLICANT: HUGHES, Richard
; APPLICANT: HUGHES, Richard
; TITLE OF INVENTION: VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF
; CURRENT APPLICATION NUMBER: US 60/176,293
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR PILING DATE: 2000-01-18
; PRIOR PILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 29, Application US/09761636A
Patent No. US20020065218A1
Fatent No. US20020065518A1
Fatent No. US20020065518A1
Fatent No. US20020065518A1
Fatent No. US20020065518A1
Fatent No. USACKER, Steven
APPLICANT: ACHEN, Marc
APPLICANT: CENDRON, Angela
TITLE OF INVENTION, VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE OF INVENTION VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al.
CURRENT APPLICATION NUMBER: US/09/761,636A
FRICK APPLICATION NUMBER: US 60/176,293
FRICK APPLICATION NUMBER: US 60/176,293
FRICK APPLICATION NUMBER: US 60/204,590
FRICK APPLICATION NUMBER: US 60/204,590
FRICK PILING DATE: 2000-01-18
NUMBER OF SEQ 1D NOS: 34
SOFTHARE: PATENTING DATE: 2000-05-16
NUMBER OF SEQ 1D NOS: 34
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Pred. No. 3.7e-07;
2; Mismatches 0; Indels
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Pred. No. 1.5e-06;
                                                                                                                                                                                                                                                                                           2; Mismatches
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PRIOR FILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: US 60/204,590
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                       1 CASELGKSINTFCKPPC 17
                                                                                                                                                                                                                                                                                                                                                              1 CASELGRSTNSFCKPPC 17
                                                                                                                                                                                                                                           93.0%;
88.2%;
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                                                                                                                                                      ; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-32
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Best Local Similarity 82.4%;
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                                                                                                                                                                                                                                  Query Match
Best Local Similarity 88.29
Marches 15; Conservative
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US-09-761-636A-3
                                                                                                         SEQ ID NO 32
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LENGTH: 17
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US-09-956-095-3

Sequence 3, Application US/09956095

Sequence 3, Application US/09956095

Sequence 3, Application US/09956095

Sequence 3, Application US/09956095

Sequence 3, Application US/0996091

GENERAL INFORMATION:

APPLICANT: ACHEN, Marc G.

APPLICANT: STACKER, Steven A.

TITLE OF INVENTION: WASCULAR ENDOTHELIAL GROWTH FACTOR D EXPRESSION, FOR SCREENING TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR D EXPRESSION, FOR SCREENING TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR D EXPRESSION, FOR SCREENING TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR D EXPRESSION, FOR MAINTAINING FILLE OF INVENTION: UNMBER: US/09/956,095

CURRENT APPLICATION NUMBER: US/09/956,095

CURRENT APPLICATION NUMBER: 09/796,714

PRIOR APPLICATION NUMBER: 60/234,196

PRIOR APPLICATION NUMBER: 60/234,196

PRIOR FILLING DATE: 2000-09-20
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APPLICANT: ACHEN, Marc

APPLICANT: STACKER, Steven

APPLICANT: BACKER, Steven

APPLICANT: CENDRON, Angela

TITLE OF INVENTION: VEGF-D/VEGF PEPTIDOMIMETIC INHIBITOR

FILE OF INVENTION VEGF-D/VEGF PEPTIDOMIMETIC INHIBITOR

FILE REFERENCE: 1064/48505 Achen et al

CURRENT FILING DATE: 2001-01-18

PRIOR APPLICATION NUMBER: US 60/176,293

PRIOR PLILING DATE: 2000-01-18

PRIOR PLILING DATE: 2000-01-18

PRIOR PLILING DATE: 2000-01-18

PRIOR PLILING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PATENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature; OTHER INFORMATION: Amino acid residues of Vall01-Pro196 of VEGF-D US-09-761-636A-1
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0
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Amino acid residues Vall01-Thr173 of VEGF-D
                                                                                                                                                                                                                     80.0%; Score 80; DB 9; Length 73; 93.8%; Pred. No. 0.00014; rive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80.0%; Score 80; DB 9; Length 96; ilarity 93.8%; Pred. No. 0.00018; Conservative 0; Mismatches 1; Indels
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; Patent No. US20020065218A1
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                                                                                                                                                                                                                                                                                    15; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FACTOR
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                                                                                                                                    Conservative
  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-779-731-1
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ORGANISM: Homo sapiens
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                                                                                         Query Match
Best Local Similarity
Matches 15; Conserva
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Matches 15; Conserv
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US-10-044-622-1
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FILE REPERENCE: 1064/44385 MARC ACHEN
CURRENT FILING DATE: 1099-12-23

PRIOR FILING DATE: 1997-12-24

PRIOR FILING DATE: 1997-12-24

PRIOR FILING DATE: 1997-12-24

PRIOR FILING DATE: 1997-12-29

PRIOR APPLICATION NUMBER: US 60/087,392

PRIOR FILING DATE: 1998-05-29

NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ACHEN, Marc G.
APPLICANT: STACKER, Steve A.
ITLE OF INVENTION: ANTIBODIES TO TRUNCATED VEGF-D AND USES THEREOF
FILE REPERENCE: ACHEN et al-1064-44660
CURRENT APPLICATION NUMBER: US/10/779,731
CURRENT APPLICATION NUMBER: US/10/100,037
PRIOR APPLICATION NUMBER: 09/469,186
PRIOR FILING DATE: 2002-03-19
PRIOR FILING DATE: 1999-12-21
PRIOR PLILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/113,254
PRIOR PLILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/113,556
PRIOR APPLICATION NUMBER: 60/134,556
PRIOR APPLICATION NUMBER: 60/134,556
PRIOR APPLICATION NUMBER: 60/134,556
PRIOR PRIOR DATE: 1999-05-17
NUMBER OF SEQ 1D NOS: 1
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80.0%; Score 80; DB 9; Length 109;
Best Local Similarity 93.8%; Pred. No. 0.00021;
Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                Length 109;
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93.8%; Pred. No. 0.00021;
tive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/10779731 Publication No. US20040141917A1 GENERAL INFORMATION:
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
                                                                                                                                                                                                                                                                         2 ASELGKSINTFCKPPC 17
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SEQ ID NO 1
LENGTH: 109
                                                                                                                                                                                Query Match
Best Local Similarity 93.83
Matches 15; Conservative
                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ACHEN, Marc
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US-09-219-345A-1
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QUENT WATCH

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ARCHES 15, CORPUTATIVE 91.87, Pred. No. 0.00021, Indals 0, Gaps 0;

ARCHES 15, CORPUTATIVE 17, Pred. No. 0.00021, Indals 0, Gaps 0;

ARCHIGATH NO. 18001211011

DD 2 ASSIGNATHTEVER 17

ARCHIGATH NO. 1800121101A1

GREEBAL INFORMATION:

ARCHIGATH NO. 18001221101A1

GREEBAL INFORMATION:

ARCHIGATH NO. 18001221101A1

ARCHIGATH NO. 18001221101A1

ARCHIGATH NO. 1800123110A1

ARCHIGATH NO. 1800123110A1

ARCHIGATH NO. 180012AR MORBER: GOLDE, SO

TITLE OF INVESTION VINCENTE MARCHES THEREOF

FILE RESERVED TO NEGROUND MORBER: GOLDE, SO

TITLE OF INVESTION NUMBER: EARLIER FILEND MORE: 1994-11-03

COFTWARE: SCHOOL NO. 180012AR MORBER: GOLDE, SO

FILE RESERVED TO NUMBER: EARLIER FILEND MORE: 1996-11-03

COFTWARE: RELIES FILEND MORE: 1996-11-03

FILE OF INVESTION NUMBER: EARLIER FILEND MORE: 1996-11-03

FOR MORE FILEND MORBER: EARLIER FILEND MORE: 1996-11-03

SOFTWARE: SCHOOL NO. 180012AR MORBER: GOLDE, SO

MARCHES 15, CORRESTANTE OF ON MERMACHER IN SOURCE SO

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OPERATING SYSTEM: DOS

us-09-761-636a-8.open.rapb

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Search completed: September 5, 2004, 10:29:18
Job time : 47.7374 secs
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; Publication No. US20030114658A1
; Publication No. US20030114658A1
; Publication No. US20030114658A1
; APPLICANT: Marce G. ACHEN
; APPLICANT: ALTALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS: 1
; ADDRESSEE: Evenson, MCKecwn, Edwards & Lenahan P.L.L.C.
STREET: 1200 G Street, NW, Suite 700
; CITT' Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.0%; Score 80; DB 13; Length 280; ilarity 93.8%; Pred. No. 0.00051; Conservative 0; Mismatches 1; Indels
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CURRENT APPLICATION DATA:

SOUTH APPLICATION DATA:

APPLICATION NUMBER: US/10/044,622
FILING DATE: 09-Jan-2002
CLASSIFICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 08/788,812

FILING DATE: CURROWN-

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REGISTRATION NUMBER: 36,749

TELEPRINCE/DOCKET NUMBER: PF-0185 US

TELEPRINCE/DOCKET NUMBER: PF-0185

TELEPRINCE/DOCKET NUMBER: PF-0185

TELEPRINCE (15-855-0555

TELEPRINCE (15-855-0555

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/274,953
FILING DATE: 22-oct-2002
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/296,275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-044-622-1
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REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/42983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                United States of America
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APPLICATION NUMBER: 08/915,795
FILING DATE:
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STRANDEDNESS: single
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IMMEDIATE SOURCE:
LIBRARY: LUNGAST01
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Best Local Similarity
Matches 15; Conserva
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TELECOMMUNICATION INFORMATION:
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TELEFAX: (202) 628-8844
                                            TELER: N/A
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 anino acids
                                                                                                                                                                                  MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: Human Breast
                                                                                                                                                                                                                                                                                                                                                                                    2 ASELGKSTNTFCKPPC 17
                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
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Copyright (c) 1993 - 2004 Compugen Ltd.
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					ALIGNMENTS		
RESULT 1 US-09-469-186-1 US-09-469-186-1 Sequence 1, Application US/09469186 Patent No. 6363484 GENERAL INFORMATION: APPLICANT: STACKER, Steve A. TITLE OF INVENTION: ANTHRODIES TO TRU FILE REPRENCE: ACHEN et al.1064-4466 CURRENT APPLICATION NUMBER: US/09/469 CURRENT APPLICATION NUMBER: 60/113,25 EARLIER FILING DATE: 1999-12-21 EARLIER FILING DATE: 1999-12-21 EARLIER FILING DATE: 1999-12-21 EARLIER FILING DATE: 1999-12-21 SOFTWARE: PAPLICATION NUMBER: 60/134,55 CONTWARE: PAPLICATION NUMBER: 60/134,55 CONTWARE: PAPLICATION NUMBER: 60/134,55 TYPER: PAPLICATION NUMBER: 60/134,55 TYPER: PAPLICATION NUMBER: 60/134,55 TYPER: PAPLICATION NUMBER: 60/134,55 TYPER: PAPLICATION NUMBER: 60/134,55 TYPER: PAPLICATION NUMBER: 60/134,55 TYPER: PAPLICATION NUMBER: 109 TYPER: PAPLICATION NUMBER: 109 TYPER: PAPLICATION NUMBER: 109 TYPER: PAPLICATION NUMBER: 109 TYPER: PAPLICATION NUMBER: 109 TYPER: PAPLICATION NUMBER: 109 TYPER: PAPLICATION NUMBER: 109 TYPER: PAPLICATION NUMBER: 109 TYPER: PAPLICATION NUMBER: 109 TYPER: PAPLICATION NUMBER: 109 TYPER: PAPLICATION NUMBER: 109 TYPER: PAPLICATION NUMBER: 109 TYPER: PAPLICATION NUMBER: 109 TYPER: PAPLICATION NUMBER: 109 TYPER: PAPLICATION NUMBER: 109 TYPER: PAPLICATION NUMBER: 100 TYPER: PAPLICATION NUMBER: 100 TYPER: PAPLICATION NUMBER: 100 TYPER: PAPLICATION NUMBER: 100 TYPER: PAPLICATION NUMBER: 100 TYPER: PAPLICATION NUMBER: 100 TYPER: PAPLICATION NUMBER: 100 TYPER: PAPLICATION NUMBER: 100 TYPER: PAPLICATION NUMBER: 100 TYPER: PAPLICATION NUMBER: 100 TYPER: PAPLICATION NUMBER: 100 TYPER: PAPLICATION NUMBER: 100 TYPER: PAPLICATION NUMBER: 100 TYPER: PAPLICATION NUMBER: 100 TYPER: PAPLICATION NUMBER: 100 TYPER: PAPLICATION NUMBER: 100 TYPER: PAPLICATION NUMBER: 100 TYPER: PAPLICATION NUMBER: 100 TYPER: PAPLICATION NUMBER: 100 TYPER: PAPLICATION NUMBER: 100 TYPER: PAPLICATION NUMBER: 100 TYPER: PAPLICATION NUMBER: 100 TYPER: PAPLICATION NUMBER: 100 TYPER: PAPLICATION NUMBER: 100 TYPER: PAPLICATION NUMBER: 100 TYPER: PAPLICATION NUMBER: 100 TYPER: PAPLICATION NUMBER: 100 TYPER: PAPLICA	APE APE APE APE APE APE APE APE APE APE	196-1  1, Application US/09469  2. 6383484 INFORMATION: NT: ACHEN, MARC G. NT: STACKER, Steve A. FINVENTION: ANTIBODIES PERENCE: ACHEN et al.106 APPLICATION NUMBER: US/ FILING DATE: 1999-12-21 APPLICATION NUMBER: 60/ FILING DATE: 1999-05-17 APPLICATION NUMBER: 60/ FILING DATE: 1999-05-17 PERING DATE: 1999-05-17 APPLICATION NUMBER: 60/ FILING DATE: 1999-05-17  2 PARTHONG DATE: 1999-05-17 APPLICATION NUMBER: 60/ FILING DATE: 1999-05-17  3 PARTHONG SANIANG  5 PARTHONG SANIANG  8 PARTHONG SANIANG  109	on US/( CC G. ANTIBO) A et a. UDBBER 1998-1 1998-1 1998-1 1999-1 1 1 29-1	,/094691 . A. . A. mall1064 RR: US/ RR: US/ RR: 60/1 -12-21 RR: 60/1	TRUNCATED VEGF-D 469,186 ,254 ,556	AND USES THEREOF	A C
Query Match Best Local	simi	se-i ch l Similarity	80.08 93.88	0 % % % 3 %	Score 80; DB 4; Pred. No. 5e-05;	60	
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Sequence 1, Application US/09469185
; Patent No. 6531185
; Patent No. 6531185
; GENERAL INFORMATION:
APPLICANT: ACHEN, Marc G.
APPLICANT: STACKER, Steve A.
ITILE OF INVENTION: ANTIBODIES TO TRUNCATED VEGF-D AND USES THEREOF
ILLE REPERBUCE. ACHEN 1054-44660
CURRENT APPLICATION NUMBER: 60/113, 254
EARLIER APPLICATION NUMBER: 60/113, 254
EARLIER FILING DATE: 1998-12-21
EARLIER FILING DATE: 1998-12-21
EARLIER FILING DATE: 1999-05-17
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin Ver. 2.0

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APPLICATION NUMBER: US/08/915,795
FILING DATE:
CLASSIFICATION: 536
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TISSUE TYPE: Human Breast
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
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APPLICANT: Wise, Lyn M
APPLICANT: Mercer, Andrew A
APPLICANT: Savory, Loren J
APPLICANT: Savory, Loren J
APPLICANT: Stacker, Stephen B
APPLICANT: Stacker, Stephen B
APPLICANT: Fleming, Stephen B
APPLICANT: Fleming, Stephen B
TITLE OF INVENTION: VARUE BINDS AND ACTIVATES MAMMALIAN VEGF
TITLE OF INVENTION: RECEPTOR-2, AND USES THEREOF
FILE REFERENCE: Sequence Listing for 09/431,833
Fatent No. 6541008
CURRENT APPLICATION NUMBER: US/09/431,888A
CURRENT APPLICATION NUMBER: 05/09/631,888A
CURRENT APPLICATION NUMBER: 60/106,689
EARLIER APPLICATION NUMBER: 60/106,689
EARLIER APPLICATION NUMBER: 60/106,800
EARLIER APPLICATION NUMBER: 60/106,800
EARLIER FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN VET. 2.0
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Patent No. 6235713
GENERAL INPORMATION:
APPLICANT: Marc G. ACHEN
APPLICANT: Steven A. STACKER
APPLICANT: Kari ALITALO
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eveneon, McKeown, Edwards & Lenahan P.L.L.C.
STREET: 1200 G Street, NW, Suite 700
                                                                                                  Query Match

80.0%; Score 80; DB 4; Length 109;
Best Local Similarity 93.8%; Pred. No. 5e-05;
Matches 15; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                 ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45 ASELGKSTNTFFKPPC 60
                                                                                                                                                                                    2 ASELGKSTNTFCKPPC 17
                                                                                                                                                                                                                         29 ASELGKSTNTFFKPPC 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 93.8
Matches 15; Conservative
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1200 G St
CITY: Washington
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TYPE: PRT
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US-08-915-795-3
                                                            US-09-469-185-1
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Gaps
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; Patent No. 6235710:
    Patent No. 6235710:
    Patent No. 6235710:
    Patent No. 6235710:
    APPLICANT: Marc G. ACHEN
    APPLICANT: Andrew F. WILKS
    APPLICANT: Steven A. STACKER
    APPLICANT: Kari ALITALO
    TITLE OF INVENTION: GROWTH FACTOR
    NUMBER OF SEQUENCES: 1
    CORRESPONDENCE ADDRESS: 1
    CORRESPONDENCE ADDRESS: 3
    ADDRESSER: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
    STREET: 1200 G Street, NW, Suite 700
    CITY: Washington
    STREET: D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.0%; Score 80; DB 3; Length 325; 93.8%; Pred. No. 0.00015; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTY: United States of America
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,795
                                                                                                           FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPh D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/42983
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 628-8840
TELEX: N/A
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NAME: EVANS, JOSEPh D.
REGISTATION NUMBER: 26, 269
REFERENCE/DOCKET NUMBER: 1064/42983
TELECOMMUNICATION INFORMATION:
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STRANDEDNESS:
        RESULT 7
US-08-915-795-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C. STREET: 1200 G Street, NW, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20005
ZIP: 20005
MEDIUM TYPE: Robpy disk
COMPUTER: Ploppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/915,795
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Marc G. ACHEN
APPLICANT: Andrew F. WILKS
APPLICANT: Steven A. STRCKER
APPLICANT: Kari ALITALO
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        United States of America
                                                                                                                                                                                                                                                                                                                                                                                               US-08-915-795-9; Sequence 9, Application US/08915795; Patent No. 6235713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 536
ATTORNEY/ACENT INFORMATION:
NAME: EVANS, JOSEPH D.
RECISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064,
TELECHONICATION INFORMATION:
TELEPHONE: (202) 628-880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: N/A
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                         121 ASELGKSTNTFFKPPC 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||||||:|||| ||||
121 ASELGKTINIFFKPPC 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ASELGKSTNTFCKPPC 17
                                                                                                      ORIGINAL SOURCE:
TISSUE TYPE: Human Lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein ORIGINAL SOURCE: TISSUE TYPE: Mouse Lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 87.5
Matches 14; Conservative
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                     TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                              US-08-915-795-5
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Sequence 11, Application US/08795430

Sequence 11, Application US/08795430

Sequence 11, Application Grant

APPLICANT: Alitalo, Kari

APPLICANT: Joukov, Vascular Endothelial Growth Factor C (VEGF-C)

TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof

NUMBER OF SEQUENCES: 57

CORRESPONDENCES: 57

ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                         E: Evenson, McKeown, Edwards & Lenahan P.L.L.C. 1200 G Street, NW, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Parentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,795
                                                                                                                                                                                                                                                                                                                                           COUNTRY: United States of America ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0. V
                                          GENERAL INFORMATION:
APPLICANT: Marc G. ACHEN
APPLICANT: Andrew F. WILKS
APPLICANT: Steven A. STACKER
APPLICANT: Kari ALITALO
ITITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwar
                                                                                                                                                                                                                                                                                                                                                           United States of America
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Sequence 8, Application US/08915795
Patent No. 6235713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFRENCE/DOCKET NUMBER: 1064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 ASELGKTTNTFFKPPC 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGIH: 358 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE TYPE: Mouse Lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: N/A
INPORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 536
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                              STREET: 1200 G St
CITY: Washington
STATE: DC
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Gaps
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MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMpatible COMPUTER: IBM PC COMpatible COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                   Patentin Release #1.0, Version #1.30
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/601,132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 59; DB 4;
Pred. No. 0.29;
                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:

PAPLICATION NUMBER: 08/795,430
FILING DATE: 05-FEB-1997
APPLICATION NUMBER: PCT/F196/00427
FILING DATE: 01-0401996
APPLICATION NUMBER: 08/61,53
FILING DATE: 28-JUN-1996
APPLICATION NUMBER: 08/601,132
FILING DATE: 14-FEB-1996
APPLICATION NUMBER: 08/510,133
FILING DATE: 12-JAN-1996
APPLICATION NUMBER: 08/510,133
FILING DATE: 12-JAN-1996
APPLICATION NUMBER: 08/510,133
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Gass, David A.
REGISTRATION NUMBER: 38,153.
REFERENCE/DOCKET NUMBER: 28967/34140
TELECOMMUNICATION INPORMATION:
                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/355,700
FILING DATE: 05-No. 6361946-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Aloukov, Vladimir
TITLE OF INVENTION: Receptor Ligand
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                      CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-601-132-41
; Sequence 41, Application US/08601132
; Patent No. 6403088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 415 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.0%;
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139 EFGAATNTFFKPPC 152
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 71.4
Watches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-355-700-11
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Helsinki University Licensing
Alitalo, Kari(U.S. only)
JOUKOV, Vladimir (U.S. only)
TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
NUMBER OF SEQUENCES: Protein and Gene, Mutants Thereof, and Uses Thereof
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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Pred. No. 0.29;
1; Mismatches 3; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/795,430
                                                                                                                                                                                                                                                     PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 01-AUG-1996
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 28-JUN-1996
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/510,133
FILING DATE: 01-AUG-1995
PRIOR APPLICATION NUMBER: 08/340,011
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION NUMBER: 08/340,011
PRIOR APPLICATION NUMBER: 08/340,011
PRIOR APPLICATION NUMBER: 08/340,011
PRIOR APPLICATION NUMBER: 08/340,011
PRIOR APPLICATION NUMBER: 08/340,011
PRIOR APPLICATION NUMBER: 08/340,011
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PRIOR APPLICATION NUMBER: 08/340,011
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PRIOR APPLICATION NUMBER: 08/340,011
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PRIOR APPLICATION NUMBER: 08/340,011
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REFERENCE/DOCKET NUMBER: 28967/33691
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/09355700 Patent No. 6361946 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELDEAL:
TELEFAX: 312/-
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
""PE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.0%;
71.4%;
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Best Local Similarity 71.4'
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-08-795-430-11
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Query Match
Best Local Similarity 71.4%
Matches 10; Conservative
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TOPOLOGY: li
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US-08-795-430-13
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Pred. No. 0.29;
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6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: CLICAGO SEALS TOWEL, 233 SOUTH MACKET DILYON COUNTRY: United States of America CONTRY: United States of America ZIP: G606-6402

COMPUTER READABLE FORM: MEDIUM TYRE: IBM PC COMPATIBLE PORM: MEDIUM TYRE: BM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOUTWARE: PAPELICATION NUMBER: US/08/671,573B FILING DATE: 28-JUN-1996
FILING DATE: 28-JUN-1996
FILING DATE: 14-FEB-1996
FRIOR APPLICATION NUMBER: 08/501,132
FILING DATE: 12-FEB-1996
FRIOR APPLICATION DATA: APPLICATION NUMBER: 08/510,133
FILING DATE: 12-MON-1996
FRIOR APPLICATION NUMBER: 08/510,133
FILING DATE: 12-MON-1996
FRIOR APPLICATION NUMBER: 08/510,133
FILING DATE: 11-MG-1995
ATTORNEY/AGENT INFORMATION: NAME: GASS, DAVIG A. REFERENCE/DOCKET NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 38,153
                                                                                                                                                                                                                                                                                                                                                             Mismatches
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28113/33118
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6480
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APPLICANT: Joukov, Vladimir
ITILE OF INVENTION: Receptor Ligand
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 41, Application US/08671573B Patent No. 6645933 GENERAL INFORMATION:
                                                                                                      TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                  Query Match 59.0%;
Best Local Similarity 71.4%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            139 EFGAATNTFFKPPC 152
                                                                                                                                                                                        j. LENGTH: 415 amino acids

j. TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-601-132-41
                                                                                                                                                                                                                                                                                                                                                                                                       4 ELGKSTNTFCKPPC 17
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    312/474-6300
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
US-08-671-573B-41
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TELEX: 2
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Sequence 13, Application US/08795430

Sequence 13, Application US/08795430

Patent No. 6130071

GENERAL INFORMATION:

APPLICANT: Alitalo, Kari

APPLICANT: Joukov, Vladimir

TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)

TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America
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                                                      Gaps
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     Length 415;
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                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,430
  DB 4;
                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: PCT/F196/00427
FILING DATE: 01-AUG-1996
PRIOR APPLICATION NUMBER: 08/71,573
FILING DATE: 28-UTN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/601,132
FILING DATE: 14-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/58,895
FILING DATE: 12-OAN-1996
PRIOR APPLICATION NUMBER: 08/510,133
FILING DATE: 01-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/510,133
FILING DATE: 01-AUG-1995
PRIOR APPLICATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28967/33691
TELECOMMUNICATION:
REFERENCE/DOCKET NUMBER: 28967/33691
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
  Score 59;
Pred. No.
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ER: 28967/33691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
59.0%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 13:
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|139 EFGAATNTFFKPPC 152
                                                                                                  4 ELGKSTNTFCKPPC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 312/474-6300
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Query Match
Best Local Similarity
Matches 10; Conserv
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                                   US-09-355-700-59
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                                                                                                                                                                                                         APPLICANT: Ludwig Institute for Cancer Research
Helsinki University Licensing
Alitalo, Kari(U.S. only)
Joukov, Vladimir (U.S. only)
TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
Protein and Gene, Mutants Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Chicago
STATE: 11linois
COUNTRY: United States of America
ZIP: 6060-640.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PLOPSY MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/355,700
FILING DATE: 05-NO. 6361946-1999
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 418; 0.29;
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APPLICATION NUMBER: 08/795,430

FILING DATE: 05-EBB-1997

APPLICATION NUMBER: PCT/F196/00427

FILING DATE: 01-AUG-1996

APPLICATION NUMBER: 08/671,573

FILING DATE: 28-UNH-1996

APPLICATION NUMBER: 08/601,132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 14-FEB-1996
APPLICATION NUMBER: 08/585, 895
RILING DATE: 12-JAN-1996
APPLICATION NUMBER: 08/510,133
FILING DATE: 01-AUG-1995
APPLICATION NUMBER: 08/340,011
FILING DATE: 14-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 13: US-09-355-700-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 59;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Gase, David A.
REGISTRATION NUMBER: 38,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: TELECOMMUNICATION:
                                                                                                                         US-09-355-700-13
; Sequence 13, Application US/09355700
; Patent No. 6361946
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 418 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.0%;
                      142 EPGATTNTFFKPPC 155
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ELGKSTNTFCKPPC 17
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Best Local Similarity 71.4
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                          RESULT 13
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APPLICANT: Ludwig Institute for Cancer Research
Helsinki University Licensing
Alitalo, Kari(U.S. only)
Joukov, Vladdimir (U.S. only)
TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGP-C)
Protein and Gene, Mutants Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·.
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                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
                                                                                                                                                                                                                                                                                                                                                                                                SITREET: BJOS SEATS TOWER, 233 SOUTH WACKET DILVED CITY: Chicago STATE: 111inois COMPUTRY: United States of America COUNTRY: United States of America CONTRY: United States of America CONTRY: United States of America COMPUTER: EADABLE FORM:

MEDIUM TYPE: Floppy disk CONTRYER: IBW PC COMPATIBLE SYSTEM: PC-DOS/MS-DOS SOFTWARR: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/355,700 FILING DATE: 05-MO: 6361969 CLASSIFICATION DATA:

APPLICATION NUMBER: US/09/35 APPLICATION NUMBER: PCT/F196/00427 FILING DATE: 12-MO: 1996 APPLICATION NUMBER: 08/61,573 FILING DATE: 12-MO: 1996 APPLICATION NUMBER: 08/61,133 FILING DATE: 12-MO: 1996 APPLICATION NUMBER: 08/61,133 FILING DATE: 11-MO: 1995 APPLICATION NUMBER: 08/510,133 FILING DATE: 11-MO: 1994 ATTORNEY/AGENT INFORMATION:

WAME: GABS: DATIGN APPLICATION NUMBER: 08/510,133 FILING DATE: 14-NOV-1994 ATTORNEY/AGENT INFORMATION:

WAME: GABS: DATIGN APPLICATION NUMBER: 08/510,133 FILING DATE: 14-NOV-1994 ATTORNEY/AGENT INFORMATION:

WAME: GABS: DATIGN APPLICATION NUMBER: 08/510,133 FILING DATE: 14-NOV-1994 ATTORNEY/AGENT INFORMATION:

WAME: GABS: DATIGN APPLICATION NUMBER: 08/510,133 FILING DATE: 14-NOV-1994 ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: 28967/34140
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: not relevant
; Sequence 59, Application US/09355700; Patent No. 6361946; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 160 amino acids
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INFORMATION FOR SEQ ID NO: 59:
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72 EFGVATNTFFKPPC 85
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RESULT 15

142 EFGATTNTFFKPPC 155

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US-04-411-888-7

US-04-411-888-7

Eaquence No. 6541008

GENERAL INFORMATION:

APPLICANT: Wise, LAN M

APPLICANT: Savory, Loreen J

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APPLICANT: Savory, Loreen J

FITLE OF INVENTION: VASCULAR ENOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF

TITLE OF INVENTION: VASCULAR ENOTHELIAL GROWTH FACTOR-LIKE PROTEIN VEGF

TITLE OF INVENTION: VASCULAR ENOTHELIAL GROWTH FACTOR-LIKE PROTEIN NUMBER: 105/09/431,883

TITLE OF INVENTION: VASCULAR ENOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF

TITLE OF INVENTION: VASCULAR ENOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF

TITLE OF INVENTION WIMBER: 60/106,689

EARLIER FILING DATE: 1999-11-02

EARLIER FILING DATE: 1998-11-03

NUMBER OF SEQ ID NO 7

EARLIER PETALING DATE: 1998-11-03

SOFTWARE: PATENTION WIMBER: 60/106,800

SOFTWARE: PATENTIAL OF THE PROTEIN OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENTIAL OF THE PATENT
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US-09-431-888-7
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Search completed: September 5, 2004, 10:21:58 Job time: 16.1111 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

September Run on:

5, 2004, 09:47:29; Search time 6.90909 Seconds (without alignments) 125.302 Million cell updates/sec

US-09-761-636A-9 55

1 CCNEESLIC 9 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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16K vascular endot	placental growth f	probable G1-S-sne	mucin 5ac - mouse	Cysteine proteinas	much 5AC (cloud	ubiquitin-protein	ubiquitin-protein	nolvketide synthas	hynothetical prote	probable unclean	probable phase ant	nlatelet-derived a	Datelet-devised a	Datelet-derived a	platelet-derived g
D49530	A56125	T39386	S59521	G86232	S53362	JC1254	A38564	PN0637	T42421	T50074	AD0255	JN0248	A37359	B28964	A48851
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148	158	228	354	416	477	1058	1058	4427	351	1778	129	166	196	196	196
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63	63	63	63,6	63	63	63	63	63	62	62	61	61	61	61.8	61
35	35	35	35	35	35	35	35	35	34.5	34.5	34	34	34	34	34
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1 A33787 A33787 A33787 C. Associate and othelial growth factor (version 1) - bovine C. Species: Bos primigenius taurus (cattle) C. Species: Bos primigenius taurus (cattle) C. Species: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 05-Nov-1999 C. Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 05-Nov-1999 C. Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 05-Nov-1999 R. Tischer, E.; Gospodarowicz, D.; Mitchell, R.; Silva, M.; Schilling, J.; Lau, K.; Crisr Biochem. Biophys. Res. Commun. 165, 1198-1206, 1989 A; Feteror anothelial growth factor: a new member of the platelet-derived growth A; Residues: A33787 A; Maccession: A33787 A; Residues: 1-120 criss A; Cross-references: GB:M33750; NID:g163810; FIDN:AAA30805.1; PID:g163811 C, Keywords: alternative splicing Query Match Best Local Similarity 77.8*; Pred, No. 14; Matches 7: Conservative No. 1.4; Matches 7: Conservative No. 1.4; Matches 7: Conservative No. 1.4;
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vascular endothelial growth factor homolog A2R, 14.7K - Orf virus

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81.8%; Score 45; DB 2; Length 133; 77.8%; Pred. No. 1.5; tive 1; Mismatches 1; Indels Best Local Similarity 77.8 Matches 7; Conservative Query Match

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Gaps

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1 CCNEESLIC 9 à d

70 CCNDESLEC 78

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C;Date: 03-Feb-1994 #sequence revision 03-Feb-1994 #text_change 05-Nov-1999
C;Accession: B44881; A43351; A61029
R;Breier, G.; Albrecht, U.; Sterrer, S.; Risau, W.
Byelopment 114, 521-532, 1992
A;Title: Expression of vascular endothelial growth factor during embryonic angiogenesis A;Reference number: A44881; MUD:92274860; PMID:1592003
                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-190 < RBES
A; Residues: 1-190 < RBES
A; Residues: 1-190 < RBES
A; Cross-references: GB:S38083; NID:g249858; PIDN:AAB22253.1; PID:g249859
A; Experimental source: embryo
A; Note: sequence extracted from NCBI backbone (NCBIN:107622, NCBID:107623)
R; Claffey, K. P.; wilkison, W.O.; Spiegelman, B.M.
J; Biol. Chem. 267, 16317-16322, 1992
A; Title: Vascular endothelial growth factor. Regulation by cell differentiation and act
A; Reference number: A43351; MUID:9235593; PMID:1644816
A; Reference number: A43351
A; Molecule type: mRNA
A; Residues: 1-116, ER, 119-190 < CLA>
A; Residues: 1-116, ER, 119-190 < CLA>
A; Residues: 1-116, ER, 119-190 < CLA>
A; Residues: 1-116, ER, 119-190 < CLA>
A; Residues: 1-116, ER, 119-190 < CLA>
A; Residues: 1-116, ER, 119-190 < CLA>
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A; Residues: 1-116, ER, 119-190 < CLA>
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A; Residues: 1-116, ER, 119-190 < CLA>
A; Residues: 1-116, ER, 119-190 < CLA>
A; Residues: 1-116, ER, 119-190 < CLA>
A; Residues: 1-116, ER, 119-190 < CLA>
A; Residues: 1-116, ER, 119-190 < CLA>
A; References: 4, 53-59, 1990
A; Title: Conditioned medium from mouse sarcoma 180 cells contains vascular endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Keywords: alternative splicing; angiogenesis; dimer; disulfide bond; glycoprotein; mi
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A;Title: Amino acid and cDNA sequences of a vascular endothelial cell mitogen that is h A;Title: Amino acid and cDNA sequences of a vascular endothelial cell mitogen that is h A;Accession: A35987; MUID:90207249; PMID:2320579
A;Accession: A35987
A;Status: preliminary
A;Accession: A35987
A;Accession: A35987
A;Cross-references: GB:M32167; NID:g204287; PIDN:AA41211.1; PID:g204288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glioma-derived vascular endothelial cell growth factor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Nov-1990 #sequence_revision 16-Nov-1990 #text_change 05-Nov-1999
C;Accession: A35987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.4%; Score 42; DB 2; Length 190; llarity 66.7%; Pred. No. 6.3; Conservative 2; Mismatches 1; Indels
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Pred. No.
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Best Local Similarity 66.7%;
Matches 6; Conservative
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85 CCNDEALEC 93
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Matches 6, Conserv
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 27-190 <715>
A;Cross-references: GB:M31836; NID:g163808; PIDN:AAA30804.1; PID:g163809
B;Ferrara, N.; Henzel, W.J.
B;Jochem. Biophys. Res. Commun. 161, 851-858, 1989
A;Title: Pituitary Follicular cells secrete a novel heparin-binding growth factor specif
A;Reference number: A33255; MUID:89286596; PMID:2735925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Molecule type: mRNA
A,Residues: 1-190 cLEU>
A;Cross-references: GB:M32976; NID:g163006; PIDN:AAA30502.1; PID:g163007
R;Tischer, E.; Gospodarowicz, D.; Mitchell, R.; Silva, M.; Schilling, J.; Lau, K.; Crisp
Biochem. Biogen. Biochem. 165, 1198-1206, 1989
A;Title: Vascular endothelial growth factor: a new member of the platelet-derived growth
A;Reference number: A33787; MUID:9012125; PMID:2610687
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                                                                                                                                                                                                                                  (domestic sheep)
#text_change 05-Nov-1999
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A;Cross-references: EMBL:X89506; NID:g899350; PIDN:CAA61677.1; PID:g899351
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                                                                                                                                                                                     vascular endothelial growth factor-1 precursor - mouse C;Species: Mus musculus (house mouse)
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Pred. No. 1.7;
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Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity
Matches 7; Conserv
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A;Status: nucleic acid sequence not shown A;Molecule type: mRNA
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A; Molecule type: mRNA
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A; Reference number: A44881; MUID:92274860; PMID:1592003
A; Reference number: A44881; MUID:92274860; PMID:1592003
A; Accession: A44881
A; Molecule type: mRNA
A; Residues: 1-214 - RBRE>
A; Cross-references: GB:S37052; NID:g249856; PIDN:AAB22252.1; PID:g249857
A; Experimental source: embryo
A; Note: sequence extracted from NCBI backbone (NCBIN:104677, NCBIP:104678)
A; Molecule type: mRNA
A; Residues: 1-140, 209-214 - RBR2>
A; Cross-references: GB:S38100; NID:g249860; PIDN:AAB22254.1; PID:g249861
A; Note: sequence extracted from NCBI backbone (NCBIN:107624, NCBIP:107625)
A; Cross-references: GB:S38100; NID:g249860; PIDN:AAB22254.1; PID:g249861
A; Note: sequence extracted from NCBI backbone (NCBIN:107624, NCBIP:107625)
B; Clauss, M; Gerlach, M; Gerlach, H; Brett, J; Wang, F; Familletti, P.C.; Pan, Y.C.
J; Exp. Med. 172, 1535-1545, 1990
A; Title: Vascular permeability factor: a tumor-derived polypeptide that induces endothel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 27-33 <CLA>
R;Sugihara, T.; Kaul, S.C.; Mitsui, Y.; Wadhwa, R.
B;Sugihara, T.; Kaul, S.C.; Mitsui, Y.; Wadhwa, R.
Bicchim. Biophys. Acta 1224, 365-370, 1994
A;Title: Enhanced expression of multiple forms of VEGF is associated with spontaneous im A;Reference number: $52136; MUID:95101726; PMID:7803491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 27-46 <SUG>
C;Comment: Homodimers could be demonstrated for recombinant VEGF-2 but not VEGF-3.
C;Keywords: alternative splicing; anglogenesis; disulfide bond; glycoprotein; homodimer;
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-214/Product: vascular endothelial growth factor-3 #status experimental <MAT>
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A41551
A98cular endothelial growth factor 206 precursor - human
N/Alternate names: vascular permeability factor
N/Contains: vascular endothelial growth factor 121 (VEGF 121); VEGF 165; VEGF 189; VEGF C; Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          porcine vascular endothelial growth
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SS2130
vascular endothelial growth factor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
C;Date: 14-Jul-1995 #sequence_revision 23-238, 1995
R;Sharma, H.S.; Tang, Z.H.; Gho, B.C.G.; Verdouw, P.D.
Biochim. Biophys. Acta 1260, 235-238, 1995
A;Title: Nucleotide sequence and expression of the porcine vascular endothelial A;Reference number: S52130; MUID:95143284; PMID:7841203
A;Status: preliminary
A;Nolecule type: mRNA
A;Residues: 1-190 <SHA>
A;Cross-references: GB:X81380; NID:9587559; PIDN:CAA57143.1; PID:9587560
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Pred. No. 9.2;
1; Mismatches 2; Indels
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Pred. No. 6.9;
2; Mismatches
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A;Molecule type: protein
A;Residues: 27-46 <SUG>
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A;Residues: 1-141,227-232 <HOU>
R;Tischer, E.; Mitchell, R.; Hartman, T.; Silva, M.; Gospodarowicz, D.; Fiddes, J.C.; Al
J. Biol. Chem. 266, 11947-11954, 1991
A;Title: The human gene for vascular endothelial growth factor. Multiple protein forms & A;Reference number: A40454; MUID:91268072; PMID:1711045
C; Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 05-Nov-1999
C; Accession: A41551; C41551; B41551; A40454; B40454; C40454; A40079; A40080; JQ1463; JQ
R; Houck, K.A.; Ferrara, N.; Winer, J.; Cachianes, G.; Li, B.; Leung, D.W.
Mol. Endocrinol. 5, 1806-1814, 1991
A; Title: The Vascular endothelial growth factor family: identification of a fourth mole A; Reference number: A41551; MUID:92168017; PMID:1791831
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A, Residues: 1-140, NV, 227-232 <WE2>
A, Experimental Source: A, DS-Kaposi's sarcoma cell
R, Connolly, D.T., Olander, J.V., Heuvelman, D.; Nelson, R.; Monsell, R.; Siegel, N.; Hay
J. Biol. Chem. 264, 20017-20024, 1989
J. Biol. Chem. 264, 20017-20024, 1989
A, Fitcle: Human vascular permeability factor. Isolation from U937 cells.
A, Reference number: A34492, MUID:90062112; PMID:2584205
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A;Cross-references: GB:M32977; NID:g181970; PIDN:AAA35789.1; PID:g181971
A;Cross-references: GB:M32977; NID:g181970; PIDN:AAA35789.1; PID:g181971
B;Weindel, K.; Marme, D.; Weich, H.A.
Biochem. Biophys. Res. Commun. 183, 1167-1174, 1992
A;Title: AIDS-associated Kaposi's sarcoma cells in culture express vascular endothelial A;Reference number: QQ1463; MUID:92231879; PMID:1567395
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A;Residues: 1-141,227-232 <TI3>
A;Cross-references: GB:M63971; GB:M63972; GB:M63974; GB:M63975; GB:M63978
R;Keck, P.J.; Hauser, S.D.; Krivi, G.; Sanzo, K.; Warren, T.; Feder, J.; Connolly, D.T.
Science 246, 1309-1312, 1989
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A;Reference number: A40079; MUID:90069609; PMID:2479987
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A;Residues: 27-36;43-49, R';72-76,'Q',78-81;59-71 <CON>
C;Comment: The most common of several alternatively spliced forms is VEGF 165.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ¿Leung, D.W.; Cachianes, G.; Kuang, W.J.; Goeddel, D.V.; Ferrara, N. cience 246, 1306-1309, 1989
;Title: Vascular endothelial growth factor is a secreted angiogenic mitogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: A40454
A;Molecule type: DNA
A;Residues: 1-165,183-232 <TI1>
A;Cross-references: GB:M63971; GB:M63972; GB:M63973; GB:M63974; GB:M63975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-140,'N',183-232 <T12>
A;Cross-references: GB:M63971; GB:M63972; GB:M63973; GB:M63974; GB:M63975;
A;Accession: C40454
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A;Residues: 1-165,183-232 <KEC>
A;Cross-references: GB:M27281; NID:g340300; PIDN:AAA36807.1; PID:g340301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: JO1463
A;Molecule type: mRNA
A;Residues: 1-140,'N', 183-232 <WEI>
A;Cross-references: EMBL:X62568; NID:g37658; PIDN:CAA44447.1; PID:g37659
A;Experimental source: AIDS-Kaposi's sarcoma cell
                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-232 <HOU1>
A;Cross-references: GB:S85192; NID:g246155; PID:g246156
A;Accession: C41551
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RiBevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F. submitted to the Protein Sequence Database, March 1999
A; Reference number: 215184
A; Accession: T04039
A; Molecule type: DNA
A; Residues: 1-162 < BEV>
A; Cross-references: EMBL: AL049488
A; Experimental source: cultivar Columbia; BAC clone F24024
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vascular endothelial growth factor C precursor - human NyAlternate names: FLT4 ligand DHM CiSpecies: Homo sapiens (man) CiSpecies: Homo sapiens (man) CiSpecies: Homo sapiens (man) CiSpecies: 17-Apr-1996 #sequence revision 01-Nov-1996 #text_change 08-Oct-1999 CiAccession: 569207, 561795; $71443; $69208; G02659 FlyCoukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksela, BMBO J. 15, 1751, 1996 Ajritle: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is a ligand fareference number: 569207; MUID:96203094; PMID:8612600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: mucleic acid sequence not shown
A; Status: mucleic acid sequence not shown
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residuaces: 1-419 < JOUS
A; Residuaces: 1-419 < JOUS
A; Cross-references: EMBL:X94216; NID:g1177488; PIDN:CAA63907.1; PID:e221096; PID:g11820
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995
A; Note: cnly a part of the translation is shown
A; Note: this is a revision to the sequence from reference S61795
R; Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksela, B; Joukov, B; Dayoel vascular endothelial growth factor, VEGF-C, is a ligand for the Flt4 (A; Reference number: S61795; MUID:96178224; PMID:8617204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 'X',104-120 <JOU2>
R;Lee, J.; Gray, A.; Yuan, J.; Luoh, S.M.; Avraham, H.; Wood, W.I.
Rubmittee to the EMBL Data Library, December 1995
A;Description: Vascular endothelial growth factor related protein (VRP): A ligand and S
A;Reference number: S69208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: nucleic acid sequence not shown; not compared with conceptual translation
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A;Residues: 1-419 <LEE>
A;Cross-references: EMBL:U43142; NID:g1150988; PIDN:AAA85214.1; PID:g1150989
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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A; Residues: 70-419 < 00011>
A; Note: this sequence has been revised in reference S69207
A; Accession: S71443
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F;1-12/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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18;
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submitted to the EMBL Data Library, May 1996
A;Reference number: H01557
                                                                                                                                                                                                                                                                                                                                                                                                       Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                       70.9%;
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 44.*
--- 4; Conservative
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A; Introns: 67/3
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                                                                                                                                                                    A)Description: promotes fluid and protein leakage from blood vessels
C;Keywords: alternative splicing; angiogenesis; dimer; disulfide bond; extracellular pro
F;1-232/Product: vascular endothelial growth factor 206 precursor #status predicted <V20
F;1-165,133-232/Product: vascular endothelial growth factor 189 precursor #status predic
F;1-141,227-232/Product: vascular endothelial growth factor 121 precursor #status predic
F;1-26/Domain: signal sequence #status predicted <SIG>F;10/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Species: ictalurid herpesvirus 1
A;Note: host Ictalurus punctatus (channel catfish)
C;Date: 17-Aug.1992 #sequence_revision 17-Aug-1992 #text_change 08-Oct-1999
C;Accession: E36787
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A; Residues: 1-82 < DAV>
A; Cross-references: GB:M75136; NID:g331209; PIDN:AAA88116.1; PID:g331223
A; Cross-references: GB:M75136; NID:g331209; PIDN:AAA88116.1; PID:g331223
B; Davison, A.J.
Virology 186, 9-14, 1992
A; Title: Channel catfish virus: a new type of herpesvirus.
A; Reference number: A39447; MUID:92087490; PMID:1727613
A; Contents: annotation
A; Note: neither protein nor nucleic acid sequence is given
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submitted to GenBank, January 1992
A;Description: Channel catfish virus: a new type of herpesvirus.
A;Reference number: A36804
                                                                                                                                                                                                                                                                                                                                                                                                       74.5%; Score 41; DB 2; Length 232; 66.7%; Pred. No. 11; ative 1; Mismatches 2; Indels
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A,Status: translated from GB/EMBL/DDBJ
A,Nolecule type: DNA
A,Residues: 1-162 <2ID>
A,Tresidues: 1-162 <2ID>
A,Tross-references: EMBL:AF096373; NID:g3695400; PID:g3695405
A,Experimental source: cultivar Columbia
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Pred. No. 7.2;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein T9A4.2 - Arabidopsis thaliana
                                                            A,Gene: GDB:VEGF
A,Cross-references: GDB:132244; OMIM:192240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Genetics:
A;Gene: 13
C;Keywords: DNA binding; zinc finger
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Best Local Similarity
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Best Local Similarity
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                                    C;Genetics:
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Matches

ò d RESULT 13

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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 107-144 < CH3>
C; Superfamily: oxytocin-neurophysin
C; Keywords: amidated carboxyl end; glycoprotein; hormone; hypothalamus
F; 1-9/Product: Arg-vasopressin #status experimental < NF2>
F; 13-105/Product: neurophysin 2 #status experimental < NF2>
F; 107-144/Product: pituitary glycopeptide #status experimental < GCP>
F; 107-144/Product: pituitary glycopeptide #status experimental
F; 107-144/Product: amidated carboxyl end (Gly) (amide in mature form from following glyc
F; 2-66, 25-39, 33-56, 40-46, 73-85, 79-97, 86-91/Disulfide bonds: #status predicted
F; 112/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 1-144 <CHA.
R;Chauvet, J.; Chauvet, M.T.; Acher, R.
FEBS Lett. 217, 180-183, 1987
A;Title: Conformation limited proteolysis in the common neurophysin-copeptin precursor :
A;Reference number: S00009; MUID:87247214; PMID:3595848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 13-144 <CH4>
R;Chauvet, M.T.; Chauvet, J.; Acher, R.
Int. J. Pept. Protein Res. 30, 676-682, 1987
A;Title: Guinea pig MSEL-neurophysin. Sequence comparison of eight mammalian MSEL-neurogans A;Reference number: JS0300; MUID:88138574; PMID:3436704
                                                                                                                                                                                                                                                                                                                             Vasopressin / neurophysin 2 precursor - guinea pig
NyAlternate names: copetin
NyAlternate names: copetin
NyContains: Arg-vasopressin; neurophysin 2; pituitary glycopeptide
C;Species: Cavia porcellus (guinea pig)
C;Date: 15-Dec-1988 #sequence revision 15-Dec-1988 #text_change 06-Sep-1996
C;Date: 15-Dec-1988 #sequence revision 15-Dec-1988 #text_change 06-Sep-1996
C;Caccesion: A29101; S00009; JS0300; A2830
R;Chauvet, M.T.; Rouille, Y.; Chauvet, J.; Acher, R.
FBBS Lett. 210, 40-44, 1987
A;Title: Guinea pig neurohypophysial hormones. Peculiar processing of the three-domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 13-105 < CH2>
A; Note: 93-Ala was also found
K; Chauvet, M.T.; Chauvet, J.; Acher, R.
FEBS Lett. 197, 169-172, 1986
A; Title: Guinea pig copeptin. The glycopeptide domain of the vasopressin precursor.
A; Reference number: A23630; MUID:86136563; PMID:3081370
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 34;
2; Mismatches 1; Indels
                                                              Indels
                                                              ;;
                          Pred. No. 27;
                                                       5
                   62.58;
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                                                    5; Conservative
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                          Best Local Similarity
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A23630
                                                    Matches
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Vasopressin / neurophysin 2 precursor - finback whale (tentative sequence) (fragment)
NYOHIRE
N'SODITAINS: APE-Vasopressin, neurophysin 2
C'Species: Baldaenoptera physalus (finback whale, common rorqual)
C'Species: Baldaenoptera physalus (finback whale, common rorqual)
C'Accession: Baldaenoptera physalus (finback whale, common rorqual)
C'Accession: Baldarion of finback wh. T.
Nature 201, 191-192, 1964
A.Title: Isolation of finback whale oxytocin and vasopressin.
A.Reference number: A93147
A.Accession: B93147
A.Molecule type: protein
A.Residues: 1-9 <ACH>
R.Acher, R.
R.Chauvet, M.T.; Codogno, P.; Chauvet, J.; Acher, R.
R.Chauvet, M.T.; Codogno, P.; Chauvet, J.; Acher, R.
R.Chauvet, B. 91-93, 1978
A.Atitle: Phylogeny of neurophysins. Complete amino acid sequence of whale (Balaenoptera A.Reference number: A91447; MUID:78148313; PMID:639997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acid sequence of horse MSEL-neuro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: A91447
A;Molecule type: protein
A;Residues: 13-107 <CRA>
A;Note: some residues may have been positioned only by homology with other neurophysins C;Comment: Glycine is placed at 10 and X's at 11 and 12 by homology with the complete se C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Description: vasopressin is a hypothalmic peptide hormone that is an antidiuretic and
F;13-102/Domain: propeptide #status predicted <PRO> F;103-419/Product: vascular endothelial growth factor C #status experimental <MAT>
                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C,Superfamily: oxytocin-neurophysin
C;Keywords: hormone; hypothalamus
F;7-51,10-24,18-41,25-31,58-70,64-82,71-76/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                  neurophysin 2 - horse (tentative sequence) (fragment)
C;Species: Equus caballus (domestic horse)
C;Date: 22-May-1981 #sequence_revision 22-May-1981 #text_change 31-Mar-2000
C;Accession: A01444
R;Chauvet, M.T.; Codogno, P.; Chauvet, J.; Acher, R.
A;Title: Phylogeny of the neurophysins: complete amino acid sequence of horse
A;Reference number: A01444; MUID:77246829; PMID:891988
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                  Score 39; DB 2; Length 419;
Pred. No. 36;
                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.3%; Score 37; DB 1; Length 92; 62.5%; Pred. No. 24; 1; Indels ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                             0; Mismatches
                                                                                              70.9%;
                                                                                                                                                             6; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                               165 CCNSEGLOC 173
                                                                                                                                                                                                                       1 CCNEESLIC 9
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CCNDESCV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein A; Residues: 1-92 < CHA>
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                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A01444
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5, 2004, 10:01:19

Search completed: September Job time : 7.90909 secs

C; Superfamily: oxytocin-neurophysin C; Superfamily: oxytocin-neurophysin C; Keywords: amidated carboxyl end; glycoprotein; hormone; hypothalamus F;1-9/Product: Agr-vasopressin #status experimental <NAS> F;13-107/Product: neurophysin 2 #status experimental <NF2> F;1-6/Disulfide bonds: #status experimental F;9/Modified site: amidated carboxyl end (Gly) (amide in mature form following glyc F;22-66,25-39,33-56,40-46,73-85,79-97,86-91/Disulfide bonds: #status predicted

ein for vasopressin

67.3%; Score 37; DB 1; Length 107;

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

September 5, 2004, 09:38:39; Search time 4.09091 Seconds (without alignments)
114.554 Million cell updates/sec Run on:

US-09-761-636A-9 55 1 CCNEESLIC 9

Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	04391R Woman Contraction	O35251 ratting nous			_		P97946 mis misculii	-		-		_			035757 rattus norv	_					P01184 balaenonter						-		arabidonei	harterionh			۴.	
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SUMMARIES	ID	VEGD HUMAN	VEGD_RAT	VEGH ORFN2	VEGA SHEEP	VEGA CAVPO	VEGA BOVIN	VEGD MOUSE	VEGA_MOUSE	VEGA_RAT	VEGA_HORSE	VEGA_PIG	VEGA_CANFA	VEGA HUMAN	VG13 HSVI1	VEGC RAT	VEGC MOUSE	VEGC HUMAN	CX3A CONOU	PLGF BOVIN	NEUZ HORSE	NEU2 BALPH	NEU2 CAVPO	NEU2 SHEEP	NEU2 HUMAN	NEUZ BOVIN	NEU2 PIG	VEGA_MESAU	RC23 ARATH	RC24 ARATH	Y53 BPT3	PLGF HUMAN	YAMB SCHPO	TXN4 CELHA	
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ф	Query Match	100.0	φ.	81.8	81.8	81.8	81.8	81.8	76.4	76.4	74.5	74.5	74.5	74.5	72.7	70.9	70.9	70.9	69.1	69.1	67.3	67.3	67.3	67.3	67.3	67.3	67.3	67.3	65.5	65.5	65.5	65.5	65.5	63.6	
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P52585 orf virus (P49764 mus musculu Q63434 rattus norv P52582 gallus gall Q05634 strongyloce Q9byh homo sapien P22314 homo sapien Q02053 musculu Q02053 musculu	V25504 Officiagus Q05470 bacillus su Q9utk4 schizosacch P83303 selenocosmi
VEGH_ORFN7 PLGF_RAT VEGA_CHICK FASC_CTRPU SZ6L_HUMAN UBA1_HUMAN UBA1_RADE	PKSL BACSU N189 SCHPO TXH4 SELHU
1488 1158 1158 1158 1158 1158 1158 1158	4427 1 1778 1 35 1
6033.6	63.6 62.7 61.8
	35 34.5 34
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4 4 4 6 4 4 7

## ALIGNMENTS

HUMAN STANDARD; PRT; 354 AA.  28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last sequence update) 10-OCT-2003 (Rel. 42, Last sequence update) Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced prowth factor) (RIGF).  FIGF OR VEGFD.  Homo sapiens (Human).  Homo sapiens (Human).  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	SEQUENCE FROM N.A. TISSUE-Lung, MEDIALINE-931349118, PubMed=9205122; MEDIALINE-931349118, PubMed=9205122; MEDIALINE-931349118, PubMed=9205122; MOIGCULAR Cloning of a novel vascular endothelial growth factor, VEGF-D."; Genomics 42:483-488 (1997). [2] SEQUENCE FROM N.A. TISSUE-Lung; MEDIALINE-98140120; PubMed=9479493; Rocchigiani M., Lestingi M., Luddi A., Orlandini M., Franco B., MEDIALINE-98140120; Cutfardi O., Oliviero S.; "Human FIGF: cloning, gene structure, and mapping to chromosome Xp22.1 between the FIGA and the GRPR genes."; [3]	SEQUENCE FROM N.A.  Achen M.G., Jeltsch M., Kukk E., Maekinen T., Vitali A., Wilks A.F.,  Achen M.G., Jeltsch M., Kukk E., Maekinen T., Vitali A., Wilks A.F.,  Alitalo K., Stacker S.A.,  Alitalo K., Stacker S.A.,  Tyosine kinasee VEGF receptor 2 (Flk1) and VEGF receptor 3 (Flt4).";  Proc. Natl. Acad. Sci. U.S.A. 95:548-553(1998).  [4]  TISSUENCE FROM N.A.  TISSUE-Lung;  MEDLINE=22388257; PubMed=12477932;	A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., A Altschul S.F., Zeeberg B., Buetow K.H., Schemen C.M., Schuler G.D., A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., A Stapleton M., Soares M.B., Donaldo M.F., Casavant T.L., Scheetz T.E., A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Halpk S.W., A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.
STANDAE STANDAE (Rel. 41, (Rel. 42, othelial g C) (FIGF). (Human). (Human).	( N.A. 1118; Pubm 1118; Pubm 122u JI., 100ning of 183-488(19 1 N.A. 1, Lestin 1 Labio A., cloning, A. 1GA and ti	1 N.A. 549; Pubm eltsch M. ercker S. othelial see VEGF cad. Sci. N.A.	L., Feinge , Collins , Collins Jordan H. Marusine Soares M. J., Marullano h. Worley K.C. , Mural P.J.
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SULGD	RR RR RR RR RR RR RR RR RR RR RR RR RR	RRY RRA PRESENT RRA PRESENT CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CO	RA RA B RA B RA B RA B RA B RA B RA B R

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                                                                                                                                                                                                                                MIM; 300091; -... Gextracellular space; TAS. GOOSTIS: C:extracellular space; TAS. GOOSTIS: P:platelet-derived growth factor receptor bin. ..; TAS. GO; GO:0005102; F:receptor binding; TAS. GO; GO:0005102; F:receptor binding; TAS. Interpre: prositive regulation of cell proliferation; TAS. Interpre: prositive regulation of cell proliferation; TAS. Interpre: prositive regulation. Factor. FRG00072; PD growth_factor. FRG00073; PD growth_factor. From FRG0341; PDGF; PDGF: PPCDOM; PD001629; PD growth_factor; 1. SM00141; PDGF: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oclon, and pancreas.

PTW: Undergoes a complex proteolytic maturation which generates a variety of processed secreted forms with increased activity toward variety of processed secreted first form an antiparallel homodimer linked by disulfide bonds before secretion. The fully processed VEGF-D is composed mostly of two VEGF homology domains (VHDs) bound by non-covalent interactions.

SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SMUUL41; FLOE, . . .
PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_1; 1.
Anglogenesis; Mitogen; Growth factor; Glycoprotein; Signal; Repeat; Cleavage on pair of basic residues; Multigene family.
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                    MEDLINE=20011413; PubMed=10542248;
Stacker S.A., Stenvere K.L., Caesar C., Vitali A., Domagala T.,
Nice E.C., Roufail S., Simpson R.J., Moritz R., Karpanen T.,
Alitalo K., Achen M.G.;
                                                                                                                                                   PROCESSING, AND SEQUENCE OF 89-94; 100-105 AND 206-213.
                                                                                                human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Y12867; CAA73371.1; JOINED.
EMBL; Y12866; CAA73371.1; JOINED.
EMBL; Y12869; CAA73371.1; JOINED.
EMBL; Y12870; CAA73371.1; JOINED.
EMBL; AJ000185; CAA03942.1; --
EMBL; BC027948; AAA27948.1; --
HSSP; P15622; JVPP.
Genew; HGNC:3708; FIGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Y12864; CAA73371.1; -...EMBL; Y12865; CAA73371.1; JOINED. EMBL; Y12866; CAA73371.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D89630; BAA24264.1; -. EMBL; Y12863; CAA73370.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 une by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            variety of processed secreted forms with increased activity toward VEGFR.3 and VEGFR.2. VEGF.D first form an antiparallel homodimer linked by disulfide bonds before secretion. The fully processed VEGF-D is composed mostly of two VEGF homology domains (VHDs) bound by non-covalent interactions (By similarity). SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last amnotation update)
Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                    o.
                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                              X 16 AA REPEATS OF C-X(10)-C-X-C-
OR 99 (IN A MINOR FORM).
VASCULAR ENDOTHELIAL GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 55; DB 1; Length 354; 100.0%; Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                                                                                                                                             2048D769D735173E CRC64;
                                                                                                                (APPROXIMATE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        326 AA.
                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF014827; AAB66557.1; -.
                                                                                                                                                                                                                                                                                                                                                                                    40444 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat)
      88
205
354
318
                                                                                                                2337
273
2293
318
1189
1189
1189
                                                                                                                                                                                                                                                                                                                 155
185
287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 CCNEESLIC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CCNEESLIC 9
                                                                                                                                                                                                                                                                                          145
155
185
287
354 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI TaxID=10116;
         22
89
226
222
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222
277
277
301
111
142
146
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                                                                                                                                                                                                                                                   DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                    CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VEGD RAT
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                         DOMAIN
                                                    PROPEP
                                                                                                                     REPEAT
                                                                                                                                                                                       REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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VEGD_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AR REPRESENTATION OF SECULAR PROPERTY AND SECULAR PARTY OF SECULAR PARTY OF SECULAR PARTY OF SECULAR PARTY OF SECULAR PARTY OF SECULAR PARTY OF SECULAR PARTY OF SECULAR PARTY OF SECULAR PARTY OF SECULAR PARTY OF SECULAR PARTY OF SECULAR PARTY OF SECULAR PARTY OF SECULAR PARTY OF SECULAR PARTY OF SECULAR PARTY OF SECURAR PARTY OF SECULAR PARTY OF SECULAR PARTY OF SECULAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY OF SECURAR PARTY O
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                                                                      SMART; SM00141; ruur; 1.
PROSITE; PS00249; PDGF 1; 1.
PROSITE; PS0278; PDGF 2; 1.
Angiogenesis; Mitogen; Growth factor; Glycoprotein; Signal; Repeat; Cleavage on pair of basic residues; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Orf virus (strain NZ2) (OV NZ-2).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lyttle D.J., Fraser K.M., Fleming S.B., Mercer A.A., Robinson A.J. "Homologs of vascular endothelial growth factor are encoded by the poxvirus orf virus.";
                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                           POTENTIAL.
4 X 16 AA REPEATS OF C-X(10)-C-X-C-
                                                                                                                                                            VASCULAR ENDOTHELIAL GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
-!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
                                                                                                                                                                                                                                                                                                                                                                                        89.1%; Score 49; DB 1; Length 326;
                                                                                                                                                                                                                                                                                                 INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                          37112 MW; 1261AFA373596C00 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Vascular endothelial growth factor homolog precursor.

    J. Virol. 68:84-92(1994).
    -!- FUNCTION: INDUCES ENDOTHELIAL PROLIFERATION.

                                                                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 0.12;
                                                                                                                                                                                                                (APPROXIMATE)
                                                                                                                                                                                                                                                  4 (INCOMPLETE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 AA
                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
          InterPro; IPR004153; CXCXC repeat.
InterPro; IPR000072; PD_growth_factor.
Pfam; PF0312B; CXCXC; 1.
Pfam; PF00341; PDGF; 1.
ProDom; PD001629; PD_growth_factor; 1.
SWART; SM00141; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1] SEQUENCE FROM N.A. MEDLINE=94076465; PubMed=8254780;
                                                                                                                                                                                                                                                                                                                                                                                                  77.88;
                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                            210
326
317
                                                                                                                                                                                                                                                                                                                                                                                                                                                              150 CCNEESVMC 158
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CCNEESLIC 9
                                                                                                                                                                                                                                                                                                 141
150
160
190
292
326 AA;
 HSSP; P15692; 1VPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parapoxvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEGH ORFN2
                                                                                                                                                                                                                                                            DISULFID
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                                                                                                                                                                                                                                                                                     DISULFID
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                                                                                                                                                                       PROPEP
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P52584;
                                                                                                                                                                                                            REPEAT
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                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEGH_ORFN2
                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
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EMBL; S67520; AAB29220.2; -.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Redmer D.A., Dai Y., Li J., Charnock-Jones D.S., Smith S.K.,
Reynolds L.P., Moor R.M.;
Reynolds L.P., Moor R.M.;
Reynolds L.P., Moor R.M.;
Reynolds L.P., Moor R.M.;
Garacterization and expression of vascular endothelial growth
factor (VEGF) in the ovine corpus luteum.",
J. Reprod. Ferril. 108:157-165(1996).
-! FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
endothelial cell growth. It induces endothelial cell
proliferation, promotes cell migration, inhibits apoptosis, and
induces permeabilization of blood vessels. It binds to the
VEGFRI/FIL-1 and VEGFR2/Kdr receptors and to heparan sulfate and
heparin (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer with PlGF (By similarity).
-!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Created)
10-OCT-2095 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annocation update)
Vascular endothelial growth factor A precursor (VEGF-A) (Vascular permeability factor) (VPF).
                                                                                                                                                                            POTENTIAL.
VASCULAR ENDOTHELIAL GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                    ) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
                                                                                                                                                                                                               HOMOLOG.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTEN
                                                                                                                                                                                                                                                                                                                                                                                      81.8%; Score 45; DB 1; Length 133; 77.8%; Pred. No. 0.26;
                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                        85 N-LINKED (GLCNAC. . .) (PO
14715 MW; 917C0F6883030C39 CRC64;
                                                       PRINTS; PR00438; GFCYSKNOT.
Probom; PR0016729; PD growth_factor; 1.
SMART; SM00141; PDGF_1:
PROSITE; PS00249; PDGF_1:
PR0SITE; PS50278; PDGF_2: 1.
PR0STE: PS50278; PDGF_2: 1.
PR0STE: PS50278; PDGF_2: 1.
PR0STE: PS50278; PDGF_2: 1.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 AA
                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
InterPro; IPR002400; GF cysknot.
InterPro; IPR000072; PD_growth_factor.
Pfam; PF00341; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97117958; PubMed=8958842;
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 77.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X89506; CAA61677.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovidae; Caprinae; Ovis.
NCBI TaxID=9940;
                                                                                                                                                                                                                                 78
1112
1114
61
70
85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCNDESLEC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CCNEESLIC 9
                                                                                                                                                                                                                                 36
67
71
71
61
70
85
133 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEGF OR VEGFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEGA SHEEP
                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                       DISULFID
DISULFID
                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P50412;
                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VEGA_SHEEP
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PRINTS; PR00438; GFCYSKNOT
                                                                                                                                                                                                                                                                                 VEGA BOVIN
P15691;
                                                                                      DISULFID
DISULFID
DISULFID
CARBOHYD
                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mitogen.
                                                                                                                                                                                                                                                                      VEGA BOVIN
                                                                                                                                                                                                                                                              RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JAN-1992) to the EMBL/GenBank/DDBJ databases.

-!-FUNCTION: Growth factor active in angiogenesis, and endothelial cell growth. Induces endothelial proliferation and vascular permeability (By similarity).

-!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer with PIGF (By similarity).

-!- SUBCELLILAR LOCATION: Secreted but remains associated to cells or to the extracellular matrix unless released by heparin (By
                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Vascular endothelial growth factor A (VEGF-A) (Vascular permeability
VEGF OR VEGFA.
                                                                                                                                                                                                                                                                           Gaps
                                                  Pfam; PF00341; rus; 1.

PRINTS; PR00438; GEVSKNOT.

PRODOM; P001629; PD growth_factor; 1.

SMART; SM00141; PDGF; 1.

PROSITE; PS00249; PDGF_2; 1.

PROSITE; PS0278; PDGF_2; 1.

Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal; Heparin-binding; Multigene family.

SIGNAL 1 26 BY SIMILARITY.

CHAIN 27 146 VASCULAR ENDOTHELIAL GROWTH FACTOR A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cavia porcellus (Guinea pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.
                                                                                                                                                                                                                 (POTENTIAL).
                                                                                                                                                                                                                                                                           ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
                                                                                                                                                          BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTEN
                                                                                                                                                                                                                                                  Length 146;
                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                      4E792CB557F91760 CRC64;
                                                                                                                                                                                                                                                   Score 45; DB 1;
Pred. No. 0.29;
                                                                                                                                                                                                                                                                                                                                                                            164 AA.
                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P15692; 1VGH.
InterPro; IPR0002400; GF cysknot.
InterPro; IPR000072; PD_growth_factor.
Pfam; PF00341; PDGF; 1.
   PIR; S57956; S57956.
HSSP; P15622; UVPP.
INCHEZPEO; IPR00100; GF CYSKNOt.
INCEIPFO; IPR000072; PD_GTOWth_factor.
                                                                                                                                                                                                                             17247 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M84230; AAA37057.1; -.
                                                                                                                                                                                                                                                    81.8%;
                                                                                                                                                                                                                                                    Query Match 81.8
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                             93
127
129
76
85
                                                 Pfam; PF00341; PDGF; 1
                                                                                                                                                                                                                                                                                                              85 CCNDESLEC 93
                                                                                                                                                                                                                                                                                                 σ
                                                                                                                                                                                                                              146 AA;
                                                                                                                                                                                                                                                                                                 1 CCNEESLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Bile duct;
                                                                                                                                                   27
51
82
86
76
85
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P26617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Berse B.;
                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                         DISULFID
                                                                                                                                                                                    DISULPID
                                                                                                                                                                                                                                                                                                                                                                    CAVPO
                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                     VEGA
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factor specific for vascular endothelial cells.";
Blochem. Biophys. Res. Commun. 161:851-858(1989).
-! FUNCTION: Growth factor active in anglogenesis, vasculogenesis and endothelial cell growth. It induces endothelial cell proiferation, promotes cell migration, inhibits apoptosis, and induces permeabilization of blood vessels. It binds to the vBGFR1/Flt-1 and vBGFR2/Kdr receptors and to heparan sulfate and heparin (By similarity).
-! SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      with PIGF (By similarity). SubcELLULAR LOCATION: Secreted but remains associated to cells or to the extracellular matrix unless released by heparin (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90121225; PubMed=2610687; Tischer E., Gospodarowicz D., Mitchell R., Silva M., Schilling J., Tischer E., Gospodarowicz D., Mitchell R., Silva M., Schilling J., Lau K., Crisp T., Fiddes J.C., Abraham J.A.; Lau K., Crisp T., Fiddes J.C., Abraham J.A.; derived growth factor gene family."; Biochem. Biophys. Res. Commun. 165:1198-1206(1989).
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BEDLINE=82285596; BubMed=2735925; Berrara N., Henzel W.J.; Petrait N., Henzel W.J.; Petruitary follicular cells secrete a novel heparin-binding growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Vascular endothelial growth factor A precursor (VEGF-A) (Vascular Permeability factor) (VPF).
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                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                81.8%; Score 45; DB 1; Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                           PROSITE; PSO1249; PDGF_1; 1.

PROSITE; PS50278; PDGF_2; 1.

Mitogen; Angiogenesis; Growth factor; Glycoprotein.

DISULPID 25 101 BY SIMILARITY.

DISULPID 60 103 BY SIMILARITY.

DISULPID 60 103 BY SIMILARITY.

DISULPID 50 SO INTERCHAIN (BY SIMILARITY).

DISULPID 50 SO INTERCHAIN (BY SIMILARITY).

ARROGHYD 74 74 N-LINKED (GLCNAC. . .) (PO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 27-190 FROM N.A. (ISOFORMS ALPHA AND BETA).
                                                                                                                                                                                                                                                                                                                              PEB86A81A9D5DCA4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              0.32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 0.32
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND SEQUENCE OF 27-47.
ProDom; PD001629; PD growth_factor; 1. SMART; SM00141; PDGF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90069608; PubMed=2479986;
                                                                                                                                                                                                                                                                                                                                                        19330 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 246:1306-1309(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity) .
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 77.5
Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||:||| |
59 CCNDESLEC 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CCNEESLIC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                           164 AA;
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ProDom; PD001629; PD_growth_factor; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                 VASCULAR ENDOTHELIAL GROWTH FACTOR A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleogtomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
                                                                                                                                                                   PIR; A33787; A3378.

R PIR; B40080; B40080.

HSSP, P15692, 1VGH.

InterPro; IPR00240; GF_cysknot.

R InterPro; IPR00341; PGCF; 1.

R PRIM; PR00341; PGCF; 1.

R PRIM; PR0041; PGCF; 1.

R PRIM; SM0141; PGCF; 1.

R SMAR; SM0141; PGCF; 1.

R PROSITE; PS00249; PGGF; 1.

R PROSITE; PS00278; PGGF_2; 1.

M Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal; crawin.-binding; Alternative splicing; Multigene family.
                                     SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Fibroblast;
MEDLINE-97030254; PubMed-8876195;
Orlandini M., Marconcini L., Ferruzzi R., Oliviero S.;
"Identification of a c-fos-induced gene that is related to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45; DB 1; Length 190; Pred. No. 0.37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (POT
Missing (in isoform Beta).
                                                                                                                                                                                                                                                                                                                                                        INTERCHAIN (BY SIMILARITY)
INTERCHAIN (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                               /FTId=VSP 004613.
R -> K (in isoform Beta).
                                                                                                                                                                                                                                                                                                                                                                                                                  /FIId=VSP 004614.
EDBF903E46E24789 CRC64;
                              IsoId=P15691-2; Sequence=VSP_004613, VSP_004614;
                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             358 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
          IsoId=P15691-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                             190 AA; 22310 MW;
                                                                                                                                       EMBL; M32976; AAA30502.1; -.
EMBL; M31836; AAA30804.1; -.
EMBL; M33750; AAA30805.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                190
93
127
129
76
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81
82
86
76
85
100
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                   Name=Beta;
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                                                                                                                                                                                                                                                                                                       SIGNAL
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and for commercial
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                                                                                                                                                                                                                                                                                                                                           MEDLINE=98288130; PubMed=9622638; Avantaggiato V., Orlandini M., Acampora D., Oliviero S., Simeone A.; Embryonic expression pattern of the murine figf gene, a growth factor belonging to platelet-derived growth factor/vascular endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTM: Undergoes a complex protectivity maturation which generates a variety of processed secreted forms with increased activity toward VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer linked by disulfide bonds before secretion. The fully processed VEGF-D is composed mostly of two VEGF homology domains (VHDs) bound by non-covalent interactions (By similarity).
platelet-derived growth factor/vascular endothelial growth factor
                                                                                                                                                                                    Yamada Y., Nezu J.-I., Shimane M., Hirata Y.;
"Molecular cloning of a novel vascular endothelial growth factor,
                           family.";
Proc. Natl. Acad. Sci. U.S.A. 93:11675-11680(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vertebral column.
INDUCTION: By the transcription factor c-fos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:108037; Figf.
GO; GO:0005576; C:extracellular; IDA.
                                                                                                                                                         MEDLINE=97349118; PubMed=9205122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mech. Dev. 73:221-224(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, X99572; CAA67892.1; -.
EMBL, D89628; BAA14002.1; -.
HSSP; P15692; 1VPP.
PMMA-2DPAGE; P97946; -.
                                                                                                                                                                                                                                                                 Genomics 42:483-488(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     factor family."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RECEPTOR SPECIFICITY
                                                                                                                                                                                                                                                                                            [3]
DEVELOPMENTAL STAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00341; PDGF
                                                                                                     SEQUENCE FROM N.A.
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6; Conservative
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Best Local Similarity
Matches 6; Conserv
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$$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\fra
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J. Biol. Chem. 271:3877-3883 (1996).
-!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
endothelial cell growth. It induces endothelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE OF 1-3 FROM N.A.
MEDLINE=96216498; PubMed=8632007;
Shima D.T., Kuroki M., Deutsch U., Ng Y., Adamis A.P., D'Amore P.A.;
"The mouse gene for vascular endothelial growth factor. Genomic
structure, definition of the transcriptional unit, and
characterization of transcriptional and post-transcriptional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
     SMART; SMUOL41; FULL, 1.
PROSITE; PS00249; PDGF 1; 1.
Anglogenesis; Mitogen, Growth factor; Glycoprotein; Signal; Repeat;
Clearage on pair of basic residues; Multigene family.
21 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS VEGF-1; VEGF-2 AND VEGF-3).
MEDLINE=92274860; PubMed=1592003;
Breier G., Albrecht U., Sterrer S., Risau W.;
"Expression of vascular andothelial growth factor during embryonic angiogeneis and endothelial cell differentiation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Last sequence update)
10.OCT-2003 (Rel. 42, Last annotation update)
Vascular endothelial growth factor A precursor (VEGF-A) (Vascular permeability factor) (VPF).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                 POTENTIAL.
4 X 16 AA REPEATS OF C-X(10)-C-X-C-X(1,3)-C.
                                                                                                                              VASCULAR ENDOTHELIAL GROWTH FACTOR
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0
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Claffey K.P., Wilkison W.C., Spiegelman B.M.;
Vsgcular endothelial growth factor. Regulation by cell
differentiation and activated second messenger pathways.";
J. Biol. Chem. 267:16317-16322(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              81.8%; Score 45; DB 1; Length 358; 66.7%; Pred, No. 0.69;
                                                                                                                                                                                                                                                                                                                           INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
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                                                                                                                                                                                                     (APPROXIMATE)
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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358
323
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94
211
227
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=VEGF-3; Synonyms=VEGF188;
IsoId=Q00731-1; Squence=Displayed;
Name=VEGF-1; Synonyms=VEGF184;
Isoid=Q00731-2; Squence=VSP 004626, VSP 004627;
Name=VEGF-2; Synonyms=VEGF120;
Isoid=Q00731-3; Sequence=VSP 004628;
ISOIG=Q00731-3; Sequence=VSP 004628;
ISOIG=Q00731-3; Sequence=VSP 004628;
ISOIG=Q00731-3; Squence=VSP 004
proliferation, promotes cell migration, inhibits apoptosis, and induces permeabilization of blood vessels. It binds to the vEGFRI/Flt-1 and VEGFRZ/Kdr receptors and to heparan sulfate and heparin (By similarity)
SUBUNIT: Homodimer, disulfide-linked. Also found as heterodimer SUBCELLULAR LOCATION: VEGF-1 and VEGF-2 are secreted while VEGF-3 remains cell-surface associated unless released by heparin. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            retention signal.
SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00249; PDGF 1; 1.
PROSITE; PS50278; PDGF 2; 1.
Mitogen; Anglogenesis; Growth factor; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.4%; Score 42; DB 1; Length 214; 66.7%; Pred. No. 1.4; 1; Indels ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /FTIG=VSP 004627,
Missing (In isoform VEGF-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VSP 004628.
GE -> ER (IN REF. 2).
B5540B51E4BB6E17 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U41383; -; NOT_ANNOTATED_CDS.
PIR; A44881; A44881.
PIR; B44881; B44881.
HSSP, P15692; 2VPF.
MGD; MGT:103178; Vegfa.
Interpro; IPR000072; PD_growth_factor.
Pfan; PP00341; PDOF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD001629; PD_growth_factor; 1.
SMART; SM00141; PDGF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; S38083; AAB22253.1; --
EMBL; S38100; AAB22254.1; --
EMBL; M95200; AAA40547.1; --
EMBL; U41383; -; NOT_ANNOTATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 AA;
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VEGA_RAT

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Miura N., Misumi K., Kawahara K., Nakashima M., Pukumitsu S.,
Kawabata H., Uto N., Oka T., Maruyama I., Sakamoto H.;
"Cloning of CDNa and high-level expression of equine vascular
endotherial growth factor (VBGF).";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Growth factor active in angiogenesis, and endothelial
cell growth. Induces endothelial proliferation and vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VASCULAR ENDOTHELIAL GROWTH FACTOR A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annoration update)
Vascular endothelial growth factor A precursor (VEGF-A) (Vascular PEGF OR VEGFA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Būkaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Perissodactyla, Equidae, Equus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Missing (in isoform VEGF-A164).
/FIId=VSP 004630.
Missing (in isoform VEGF-A120).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /FTIGHTORN 004631.
Missing (In isoform VEGF-A144).
/FTIGHTORN 004632.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00249; PDGF 1; 1.
PROSITE; PS50278; PDGF 2; 1.
Mitogen; Anglogenesis; Growth factor; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . ).
K -> N (in isoform VEGF-A164).
/FTId=VSP_004629.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; AAF19212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heparin-binding; Alternative splicing; Multigene family SigNAL.
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60FBB876F5304946 CRC64;
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Pred. No. 1.4;
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                                                                                                                                                                                                                                                                EMBL; AF215725; AAF19211.1; -.
EMBL; AF215726; AAF19212.1; -.
EMBL; AF22279; AAF25958.1; -.
HSSP; P15692; 1VPP.
INTERFO; IPR000072; PD_growth_factor.
Pfam; PF00341; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD001629; PD_growth_factor; 1. SRARIT; 8M00141; PDGF; 1.
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85 CCNDEALEC 93
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Q9GKR0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Glial tumor;

X MEDLINE=9521439; PubMed=7706320;

X Disalvo J., Bayne M.L., Conn G., Kwok P.W., Trivedi P.G.,

A Disalvo J., Bayne M.L., Conn G., Kwok P.W., Trivedi P.G.,

A Disalvo J., Balisi T.M., Sullivan K.A., Thomas K.A.;

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"Developmental expression of vascular endothelial growth factor in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM VEGF-A164), AND SEQUENCE OF 27-190. MEDLINE=90207249; PubMed=2320579; Corn G., Bayne M.L., Soderman D.D., Kwok P.W., Sullivan K.A., Palisi T.M., Hope D.A., Thomas K.A., The Manio acid and cDNA sequences of a vascular endothelial cell mitogen that is homologous to platelet-derived growth factor."; Proc. Natl. Acad. Sci. U.S.A. 87:2628-2633(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the
                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Mētazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  after secretion and is bound avidly by heparin and the extracellular matrix, although it may be released as a soluble form by heparin, heparinase or plasmin (By similarity).
                                                                                                                       VEGA_RAT STANDARD; PRT; 214 AA.
P16612; OSUKX7; Q9QXG7;
01-AUG-1990 (Rel. 15, Created)
28-FRB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Vascular endothelial growth factor A precursor (VEGF-A) (Vascular VEGF OR VEGFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 Isoda=15612-4; Sequence=VSP 004631;
-1- TISSUE SPECIFICITY: Expressed in the pituitary, in brain, in particularly in supraoptic and paraventricular nuclei and the choroid plexus. Also found abundantly in the corpus luteum of ovary and in kidney glomeruli.
-!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORMS VEGF-A188; VEGF-A164; VEGF-A144 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=VEGF-A164;
IsoId=P16612-2; Sequence=VSP_004629, VSP_004630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=4; Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=P16612-3; Sequence=VSP_004632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=P16612-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEGF-A120).
MEDLINE=21092309; Pubmed=11163598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arch. Oral Biol. 46:77-82(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               masseter muscle of rats.";
                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat)
85 CCNDEALEC 93
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                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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 permeability (By similarity).
--- SUBDNIT: Homodimer; disulfide-linked. Also found as heterodimer with PlGF (By similarity).
--- SUBCELLULAR LOCATION: Secreted but remains associated to cells or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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"PCR cloning of porcine cardiac vascular endothelial growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P49151; Q9GL52;

10-FBE-1996 (Rel. 33, Last sequence update)

10-OCT-2003 (Rel. 42, Last annotation update)

Vascular endothelial growth factor A precursor (VEGF-A) (Vascular vEGF OR VEGF)
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Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VASCULAR ENDOTHELIAL GROWTH FACTOR BY SIMILARITY.
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                                                                          to the extracellular matrix unless released by heparin (By
                                                                                                              SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
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MEDLINE=95143284; PubMed=7841203;
MEDLINE=95143284; PubMed=7841203;
MEDLINE=95143284; PubMed=7841203;
Medleotide sequence and expression of the porcine vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;
Multigene family.
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Pred. No. 1.9;
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INTERCHAIN (BY SIMILARITY)
N-LINKED (GLCNAC. . .) (POT
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Biochim. Biophys. Acta 1260:235-238(1995).
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InterPro; IPR000072; PD_growth_factor.
Pfam; PF00341; PDGF; 1.
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ProDom; PD001629; PD_growth_factor; 1.
SMART; SM00141; PDGF; 1.
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HSSP; P15692; 1VGH.
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66.7%;
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    gumented (NOV-2000) to the EMBL/GenBank/DDBJ databases.
    Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
    FUNCTION: Growth factor active in angiogenesis, vasculogenesis and endothelial cell growth. It induces endothelial cell growth. It induces endothelial cell migration, inhibits apoptosis, and induces permeabilization of blood vessels. It binds to the VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1 and VEGFRI/FIL-1
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VASCULAR ENDOTHELIAL GROWTH FACTOR A.
VASCULAR ENDOTHELIAL GROWTH FACTOR A.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
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VEGA_CANFA; Q9XSF4; Q9XSF5;

Q9MYV3; Q9XSF3; Q9XSF4; Q9XSF5;

28-FEB-2003 (Rel. 41, Last sequence update)

10-OCT-2003 (Rel. 42, Last annotation update)

Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Carnivora, Rissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -LINKED (GLCMAC. .) (POTENTIAL)
- A (IN REF. 2).
04D40B8D7913047F CRC64;
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PROSITE; PS50278; PDGF 2; 1.
Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB 1; Length 190;
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InterPro; 1PR0002400; GF_cysknot.
InterPro; 1PR000072; PD_growth_factor.
Pfam; PF00341; PDGF; 1.
PRINTS; PR00438; GFCYSKNOT.
ProDom; PD001629; PD_growth_factor; 1.
SMART; SM00141; PDGF; 1.
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SEQUENCE FROM N.A. (ISOFORM VEGF-188)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF318502; AAG33064.1; -. PIR; S52130; S52130.
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66.7%;
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VEGF OR VEGFA.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity)
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Scheidegger P., Weiglhofer W., Suarez S., Kaser-Hotz B., Steiner R.,
Ballmer-Hofer K., Jaussi R.;
                                                                                                                                                                                                                                                             Name=VEGF-164;
IsoId=Q9MYV3-3; Sequence=VSP_004615, VSP_004616;
SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
                                                             SEQUENCE FROM N.A. (ISOFORMS VEGF-188; VEGF-182 AND VEGF-164)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00249; PDGF 1; 1.
PROSITE; PS50278; PDGF 2; 1.
Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal; Hepzin-binding; Alternative splicing; Multigene family.
SIGNAL 1 26 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -> V (IN REF. 2).
-> S (IN REF. 2).
0AC980A158C44B27 CRC64;
                                                                                                                                                                                                       Event=Alternative splicing, Named isoforms=3;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            004616
                                                                                                                                                                                                                                                   IsoId=09MYV3-2; Sequence=VSP_004617;
                                                                                                                                                                                                                                    IsoId=Q9MYV3-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
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/FTId=VSP
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INterPro; IPRO00072; PD growth_factor.
Pfam; PF00341; PDGF; 1.
ProbOm; PD001629; PD growth_factor; 1.
SMART; SM00141; PDGF; 1.
 MEDLINE=20125516; PubMed=10661874;
                                  bearing dogs.";
Biol. Chem. 380:1449-1454(1999)
                                                                                                                                                                                                                                                                                                                                                                      EMBL; AJ133758; CAB82426.1; -.
EMBL; AF133250; AAD29684.1; -.
EMBL; AF133249; AAD29683.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF133248; AAD29682.1; -.
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                                                                                                                                                                                                                          Name=VEGF-188;
                                                                                                                                                                                                                                            Name=VEGF-182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214 AA;
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51
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                                                                                                                                                                                        similarity)
                                                                     TISSUE=Heart;
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Query Match

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66.7%; Pred. No. 2.1; ive 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol. Chem. 272:7151-7158(1997)
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MEDLINE=99096474; PubMed=9878851;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 246:1306-1309(1989).
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                 6; Conservative
                                                                  |||:| | |
85 CCNDEGLEC 93
                                             1 CCNEESLIC 9
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                              Judging L., Roque R.S.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
-- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and endothelial cell growth. It induces endothelial cell proliferation, promotes cell migration, inhibits apoptosis, and induces permeabilization of blood vessels. It binds to the VEGFRI/Filt-1 and VEGFRZ/Kdr receptors and to heparan sulfate and heparin (By similarity)
--- SUBDNIT: Homodimer; disulfide-linked. Also found as heterodimer with PIGF (By similarity).
--- SUBCELDUAR LOCATION: Secreted but remains associated to cells or to the extracellular matrix unless released by heparin (By
                                   "Vascular endothelial growth factor (VEGF) and its receptors in tumor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VASCULAR ENDOTHELIAL GROWTH FACTOR A.
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BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLORAC. ...) (POTENTIAL).
K. -> N (in isoform VEGF-164).
/FTId=VSP_004615.
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/FTId=VSP_004617.
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM VEGF206).
MEDLINE=22168017; PubMed=1791831;
HTDLACK K.A., Ferrara N., Winer J., Cachianes G., Li B., Leung D.W.;
HTDLACK VASCULAR endothelial growth factor family: identification of a fourth molecular species and characterization of alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Poltorak Z., Cohen T., Sivan R., Kandelis Y., Spira G., Vlodavsky I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Keshet E., Neufeld G., "VEGF145, a secreted vascular endothelial growth factor isoform that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92231879; PubMed=1567395; Weindel K., Marme D., Weich H.A.; "AlDS-associated Kaposi's sarcoma cells in culture express vascular endothelial growth factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1990 (Rel. 14, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Vascular endothelial growth factor A precursor (VEGF-A) (Vascular permeability factor) (VPF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N
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MEDLINE=91268072; PubMed=1711045;
Tischer E., Mitchell R., Hartman T., Silva M., Gospodarowicz D.,
Fiddes J.C., Abraham J.A.;
"The human gene for vascular endothelial growth factor. Multiple protein forms are encoded through alternative exon splicing.";
J. Biol. Chem. 266:11947-11954(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90069609; PubMed=2479987;
Keck P.J., Hauser S.D., Krivi G., Sanzo K., Warren T., Feder J.,
Connolly D.T.;
                                                                                                                                                                                                                                                                                             VEGA_HUWAN STANDARD; PRT; 232 AA.
P15672; O60720; O75875; Q16889; Q96L82; Q96NW5; Q9H1W8; Q9H1W9;
Q9UH58; Q9UL23;
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Leung D.W., Cachianes G., Kuang W.-J., Goeddel D.V., Perrara
"Vascular endothelial growth factor is a secreted angiogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM VEGF189), AND PARTIAL SEQUENCE
       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1] SEQUENCE FROM N.A. (ISOFORMS VEGF189 AND VEGF165)
2
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"Heterogeneous vascular endothelial growth factor (VEGF) isoform mRNA and receptor mRNA expression in human glomeruli, and the identification of VEGF148 mRNA, a novel truncated splice variant."; Sato J.D., Whitney R.G.; "Human cDNA for vascular endothelial growth factor isoform VEGF121."; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases. MEDLINE=98119755; PubMed=9450968; Claffey K.P., Shih S.-C., Mullen A., Dziennis S., Cusick J.L., Abrams K.R., Lee S.W., Detmar M.; Identification of a human VPFVUGF 3' untranslated region mediating Mypoxia-induced mRNA stablity."; Mol. Biol. Cell 9:469-481(1998). MEDLINE=90062112; PubMed=2584205; Connolly D.T., Olander J.V., Heuvelman D., Nelson R., Monsell R., Siegel N.T. Glander J.V., Heuvelman D., Feder J.; Human vascular permeability factor. Isolation from U937 cells."; Human vascular permeability factor. [180] E.M. Biol. Chem. 264:20017-20024(1989). Jingjing L., Xue Y., Agarwal N., Roque R.S.;
"Human Muller cells express VEGF183, a novel spliced variant of vascular endothelial growth factor.";
Invest. Ophthalmol. Vis. Sci. 40:752-759 (1999). "Identification and characterization of a new splicing variant vascular endothelial growth factor: VEGF183."; Biochim. Biophys. Acta 1443:400-406(1998). Murata H., Fukushima J., Hattori S., Okuda K., Yanagi H.; "Human cDNA for the vascular endothelial growth factor isoform SEQUENCE FROM N.A. (ISOFORM VEGF165).

Liu J., Peng X., Yuan J., Qiang B.;

"Cloning of vascular endothelial growth factor (VEGF) cDNA.";

Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. Shan Z.X., Yu X.Y., Lin Q.X., Fu Y.H., Zheng M., Tan H.H., "Cloning and identification of vascular endothelial growth isoform VEGF165."; SEQUENCE OF 23-232 FROM N.A. (ISOFORM VEGF165).
Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee
Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. TISSUE=Renal glomerulus; MEDLINE=99394945; PubMed=10464055; Whittle C.J., Gillespie K.M., Harrison R., Mathieson P.W., Williams S.; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases. Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases SEQUENCE OF 114-209 FROM N.A. (ISOFORM VEGF183) PRELIMINARY SEQUENCE OF 27-36; 43-50 AND 59-81. SEQUENCE FROM N.A. (ISOFORM VEGF148). SEQUENCE FROM N.A. (ISOFORM VEGF165). SEQUENCE FROM N.A. (ISOFORM VEGF165). SEQUENCE FROM N.A. (ISOFORM VEGF121). SEQUENCE FROM N.A. (ISOFORM VEGF165) MEDLINE=99165303; PubMed=10067980; Clin. Sci. 97:303-312(1999). TISSUE=Hemangioendothelioma; Pei D.; SEQUENCE FROM N.A. Williams S.; Jiang A., TISSUE=Retina; IISSUE=Heart; Harper S.J. VEGF165. Shan 

Murphy J.F., Fitzgerald D.J.;

"Vascular endothelial growth factor induces cyclooxygenase-dependent proliferation of endothelial cells via the VEGF-2 receptor.";

"RASEB J. 15:1667-1667(2001).

-! FANET JON: Growth factor active in angiogenesis, vasculogenesis and endothelial cell growth. It induces endothelial cell growth. It induces endothelial cell proprietation, promotes cell migration, inhibits apoptosis, and induces permeabilization of blood vessels. It binds to the VEGFR1/FIL and VEGFR2/Kdr receptors and to heparan sulfate and heparin. Neuropilin-1 binds isoforms VEGF-165 and VEGF-145.

-: SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer X-TAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 39-134.
MEDLINE-99119204; PubMed-9922142;
Wiesmann C., Christinger H.W., Cochran A.G., Cunningham B.C.,
Waichrother W.J., Keenan C.J., Meng G., de Vos A.M.;
"Crystal structure of the complex between VEGF and a receptor-blocking "Vascular endothelial growth factor: crystal structure and functional mapping of the kinase domain receptor binding site."; Proc. Natl. Acad. Sci. U.S.A. 94:7192-7197(1997). STRUCTURE BY NMR OF 34-135.
MEDLINE=97477915; PubMed=9336848;
Pairbrother W.J., Champe M.A., Christinger H.W., Keyt B.A.,
Starovasnik M.A.,
"1H, 13C, and 15N backbone assignment and secondary structure of the receptor-binding domain of vascular endothelial growth factor.";
Protein Sci. 6:2250-2260(1997). Gaps MEDLINE-98035455; PubMed-9351807; Muller Y.A., Christinger H.W., Keyt B.A., de Vos A.M.; Christinger H.W., Keyt B.A., de Vos A.M.; "The crystal structure of vascular endothelial growth factor (VEGF) refined to 1.93-A resolution: multiple copy flexibility and receptor with PIGF (By similarity).
-!- SUBCELLULAR LOCATION: VEGF121 is acidic and freely secreted.
VEGF165 is more basic, has heparin-binding properties and, although a signicant proportion remains cell-associated, most MEDLINE=97352774; PubMed=9207067; Muller Y.A., Li B., Christinger H.W., Wells J.A., Cunningham B.C., ; "Solution structure of the heparin-binding domain of vascular endothelial growth factor."; Structure 6:637-648(1998). Fiebich B.L., Jaeger B., Schoellmann C., Weindel K., Wilting C., Rochs G., Marme D., Hug H., Weich H.A.;
"Synthesis and assembly of functionally active human vascular endothelial growth factor homodimers in insect cells.";
Eur. J. Biochem. 211:19-26(1993). MEDLINE-98298440; PubMed-9634701; Falrbrother W.J., Champe M.A., Christinger H.W., Keyt B.A., Starovasnik M.A.; 74.5%; Score 41; DB 1; Length 232; 66.7%; Pred. No. 2.3; 2; Indels ive 1; Mismatches 2; Indels X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS) OF 34-135. K-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 34-135. peptide."; Biochemistry 37:17765-17772(1998). MEDLINE=21320570; PubMed=11427521; MEDLINE=93145946; PubMed=7678805; Structure 5:1325-1338(1997). STRUCTURE BY NMR OF 137-215. 6; Conservative Query Match Best Local Similarity de Vos A.M.; FUNCTION. binding.' Matches Lin S.G.; factor of

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Search completed: September
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10-OCT-2003 (Rel. 42, Last annotation update)
Vascular endothelial growth factor C precursor (VEGF-C) (Vascular endothelial growth factor related protein) (VRP) (Flt4 ligand) (Flt4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PARCHALL STRUMLER OF ANY MACHEMENT OF A STRAIN-Sprague-Dawley; TISSUB-Lung; Mandriota S.J., Pepper M.S.; Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.

-!-FUNCTION: Growth factor active in angiogenesis, and endothelial cell growth, stimulating their proliferation and migration and also has effects on the permeability of blood vessels. May function in angiogenesis of the venous and lymphatic vascular systems during embryogenesis, and also in the maintenance of differentiated lymphatic endothelium in adults. Binds and activates VEGFR-2 (FIXI) and VEGFR-3 (FIX1) receptors.

-:- SUBUNIT: Homodimer; non-covalent and antiparallel.
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                                                                                                                      Viruses; dsDNA viruses, no RNA stage; Herpesviridae; NCEl TaxID=10401;
                                                                                                                                                                                                                                Davison A.J., "Channel catfish virus: a new type of herpesvirus."; Virology 186:9-14(1992).
                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M75136; AAA88194.1; -.
EMBL; M75136; AAA88116.1; -.
BYR, E36787; E36787.
Hypothetical protein; Zinc; Zinc-finger.
SEQUENCE 82 AA; 8821 MW; 6C009A50FF8C4C67 CRC64;
                                                      01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical gene 13 zinc-binding protein.
                                  82 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 AA.
                                                                                                                                                                                                                      MEDLINE=92087490; PubMed=1727613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
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                                STANDARD;
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                                                                                                                                                                                          SEQUENCE FROM N.A.
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Best Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Fragment)
                                VG13 HSVI1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEGC RAT
                                           000166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     035757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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5, 2004, 09:56:05

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
-1- SUBCELLULAR LOCATION: Secreted.
-1- FTM: Undergoes a complex proteolytic maturation which generates a variety of processed secreted forms with increased activity toward vEGFR-3, but only the fully processed form could activate VEGFR-2. VEGFR-3, but only the fully processed form could activate VEGFR-2. VEGF-C first form an antiparallel homodimer linked by disulfide bonds. Before secretion, a cleavage occurs between arg-227 and ser-228 producing an heterotetramer. The next extracellular step of the processing removes the N-terminal propeptide. Finally the mature VEGF-C is composed mostly of two VEGF homology domains (VHDs) bound by non-covalent interactions (By similarity).
-1- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . .) (POTENTIAL)
. .) (POTENTIAL)
. .) (POTENTIAL)
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Pred. No. 2.8;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTE
N-LINKED (GLCNAC. . .) (POTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cleavage on pair of basic residues; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50278; PDGF_2; 1.
Anglogenesis; Mitogen; Growth factor; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS, PR00438; GFCYSKNOT.
ProDom; PD001629; PD_growth_factor; 1.
SMART; SM00141; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro, IPR002400; GF cysknot.
InterPro, IPR000072; PD_growth_factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF010302; AAB63248.1; -.
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Best Local Similarity
Matches 6; Conserv
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9; Search time 20.3636 Seconds (without alignments)
139.448 Million cell updates/sec
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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                                                                                            5, 2004, 09:46:09
                                                            OM protein - protein search, using sw model
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sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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sp_vertebrate:*
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sp_phage:*
sp_plant:*
sp_rodent:*
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Maximum DB seq length: 2000000000
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sp_bacteria:*
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                                                                                            Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Q8qgd7 gallus gall Q91ze4 rattus norv Q8b571 pseudocowpo Q8min0 capra hircu 097500 oryctolagus 097500 oryctolagus 091843 oryctolagus 09182 capreolus c 09mzbl ovis aries 08664 oryctolagus 09181 capreolus c 08186 capreolus c 08748 orf virus. 08098 orf virus. 042571 xenopus lae 077643 ovis aries Description SUMMARIES Q91ZE4 Q8B571 Q8MINO Q9500 Q18843 Q9N1S2 Q8MINI Q9MZB1 Q9N1S1 Q9N1S1 Q9N1S1 Q9NNB6 080GE8 042571 077643 **080GD7** Query Match Length DB 81.8 81.8 81.8 81.8 81.8 81. 81. Score Result Ño.

	0/0123 mgs muschiu 073822 brachydanio 073682 brachydanio 0912e1 rattus norv 099x39 spalax leuc 099k00 callithrix	Q8sp29 sus scrofa Q9bdp7 macaca mula Q8wmq4 sus scrofa Q8sp15 equus cabal Q8hy70 musetela vis Q951q4 felis silve	TTTEO	UJIZBA METLODES UN Q71316 Drachydanio Q91ze3 rattus norv 05/352 coturnix co Q8twk6 methanopyru Q7v416 prochloroco
13 042572 11 080UA0 11 088911 3 005458	a	6 Q8SPZ9 6 Q9BDP7 6 Q8WMQ4 6 Q8SPL5 6 Q8HY70		
6644	1441 1881 1900 1244	124 126 127 128 184	191 191 191 146 146	324 316 316 324
81.8 76.4 76.4	4.07 4.07 4.07 4.07 5.47	2.47 2.44 2.47 3.47 3.47	4 4 4 4 7 7 7 8 4 4 4 7 7 7 7 8 8 8 8 8	70.70 70.90 70.90 69.11
4444	4 4 4 4 4 3 4 4 4 4	4 4 4 4 4 4 1 1 1 1 1 1 1 1 1	4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	, , , , , , , , , , , , , , , , , , ,
11 118 119 120 120	1 2 2 2 2 2 1 2 2 4 12 2	22 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	ሉ 4 4 4 4 4 ጋ ዛ ሪ/ ሂ/ ፋ ቴ/ ኒ/

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                     Diaz-Trelles R., Rodriguez-Leon J., Kawakami Y.,
Izpisua-Belmonte J.C.;
"Expression of the chick vascular endothelial growth factor D gene
during limb development.";
Mech. Dev. 0:0-012002).
BMBL, AF479650; AAM12733.1; -.
GO, GO:0016020; C:membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0008151; P:cell growth factor activity; IEA.
GO; GO:0008151; P:cell growth factor.
Ffam; PF00341; PDGF; 1.
ProDon; PD0016529; PD growth_factor.
Promy PD016529; PD growth_factor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89.1%; Score 49; DB 13; Length 252; 88.9%; Pred. No. 0.11; live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0GF_1; 1.
0GF_2; 1.
28767 MW; 643475DAB2E72F27 CRC64;
                                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Vascular endothelial growth factor D.
                                    252 AA.
                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Conservative
                                 PRELIMINARY;
                                                                                                                                Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00141; PDGF; J
PROSITE; PS00249; PDGF
PROSITE; PSS0278; PDGF
SEQUENCE 252 AA; 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                          NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                 Q8QGD7
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Matches
RESULT 1
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Ouery Match
Best Local Similarity 77.5-
F. Conservative
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Matches 7; Conservative
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                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                              88 CCNDESQIC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CCNEESLIC 9
                                                                                                         1 CCNEESLIC 9
                                                                                                                                                                                                                                                                 Capra hircus (Goat).
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Q8MIN0
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80 BB BB
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Kirkin V., Mazitschek R., Krishnan J., Steffen A., Waltenberger J.,

Rirkin V., Mazitschek R., Krishnan J., Steffen A., Waltenberger J.,

Pepper M.S., Giannia A., Sleeman J.P.;

Rirkin V., Mazitschek B., Sleeman J.P.;

Rarization of indolinones which specifically inhibit VEGF-C-and

VEGF-D-induced activation of VEGFR-3 but not VEGFR-2.";

Rur. J. Blochem. 0:0-0(2001).

REMBI, AV032728; AAM56008:1; -.

RO; GO:0006083; F:growth factor activity; IEA.

RO; GO:000811; P:cell growth and/or maintenance; IEA.

RO; GO:000811; P:cell growth and/or maintenance; IEA.

InterPro; IPR00012; PD growth_factor.

Repan; PF00134; PDGF; 1.

RevDom; PD001429; PD growth_factor; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ueda N., Wise L.M., Stacker S.A., Fleming S.B., Mercer A.A.; "Pseudocowpox virus encodes a homolog of vascular endothelial growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudocowpox virus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 49; DB 11; Length 326;
Pred. No. 0.13;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00249; PDGF 1; 1.
PROSITE; PS50278; PDGF 2; 1.
SEQUENCE 326 AA; 37\overline{10}06 MW; D7CAEBA6C9FABB7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL. AF542070; AMO16216.1; -...
GO; GO:0016020; C:membrane; IEA.
GO; GO:00108083; F:growth factor activity; IEA.
GO; GO:0008083; F:growth factor activity; IEA.
GO; GO:0008151; P:cell growth and/or maintenance; IEA.
InterPro; IPR002040; GF_Cysknot.
Pfem; PF00341; PDGF; 1...
Pfam; PF00341; PDGF; 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Vascular endothelial growth factor-like protein.
                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
VEGF-D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152 AA
                                                326 AA
                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        89.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                PRELIMINARY;
                                                                                                                       Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150 CCNEESVMC 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CCNEESLIC 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parapoxvirus.
NCBI_TaxID=129726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                 SEQUENCE FROM N.A
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                                             Q91ZE4
Q91ZE4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        factor.
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                        RESULT 2
                                    Q91ZE4
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SEQUENCE FROM N.A.

TISSUE-Corpus luteum;

Kawate N., Tsuji M., Tamada H., Inaba T., Sawada T.;

'Changes of Messenger RNAs Encoding Vascular Endothelial Growth Factor and Its Receptors during the Development and Maintenance of Caprine Corpora Lutea.";
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae; Capra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryctolagus cuniculus (Rabbit).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                            .
                                                                                                                                          83.6%; Score 46; DB 12; Length 152; 77.8%; Pred. No. 0.26; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.8%; Score 45; DB 6; Length 65; 77.8%; Pred. No. 0.19; 1; Indels iive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Colporated (MAX-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AX114353; AAM76674.1; -...
GO; GO:0016020; C:membrane; IEA.
GO; GO:00080151; F:growth factor activity; IEA.
GO; GO:00080151; F:growth factor activity; IEA.
InterPro; IPR000072; PD_growth_factor.
From; PF00341; PDGF; 1.
Probom; PD001629; PD growth_factor:
From; PF00141; PDGF; 1.
PROSITE; PS50278; PDGF; 1.
                                                                                    F4B3956D60B37A3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 AA; 7562 MW; BA3E5384364B05E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WENTIO, 10-0CT-2002 (TrEMBLrel. 22, Created) 01-0CT-2002 (TrEMBLrel. 22, Last sequence update) 01-0CT-2003 (TrEMBLrel. 24, Last annotation update) Vascular endothelial growth factor 121 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
Vascular endothelial growth factor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 AA.
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ProDom; PD001629; PD_growth_factor; 1. SMART; SM00141; PDGF; 1. SM00121E; PS50278; PDGF; 1. SEQUENCE 152 AA; 16202 MW; F4B3956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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Inoue K., Kawabe Y., Kodama T.;
"Rabbit VEGF CDNA, partial.";
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SEQUENCE
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Q9N1S2;
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Skorjanc D., Jaschinski F., Heine G., Pette D.;

Skorjanc D., Jaschinski F., Heine G., Pette D.;

"Sequential increases in Capillarization and mitochondrial enzymes in low-frequency-stimulated rabbit muscle.",

Am. J. Physiol. 274:C810-C818(1998).

EMBL; AF022179; AAC15469.1;

HSSP; P49763; 1FZV.

GO; GO:0016083; F:growth factor activity; IEA.

GO; GO:0008151; P:cell growth and/or maintenance; IEA.

InterPro; IPR002400; GF_cysknot.

InterPro; IPR000172; PD_growth_factor.

Activity in an interpro; IPR000172; PD_growth_factor.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.

REMB1, AB020216; BAA36949.1; -.

HSSP, P49763; IFZV.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0016015; F:growth factor activity; IEA.

GO; GO:0008083; F:growth factor activity; IEA.

RO; GO:00080815; P:growth and/or maintenance; IEA.

RINTERPRO; IPRO0072; PD_growth_factor.

Rem; PF00341; PDGF; 1.

RPCODO; PD001629; PD growth_factor; 1.

REMST; SM00141; PDGF; 1.

RRCSITE; PS00249; PDGF_1: 1.

RRCSITE; PS00249; PDGF_2: 1.
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Pred. No. 0.22;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                            81.8%; Score 45; DB 6; Length 68; 77.8%; Pred. No. 0.2; Live 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                 68 AA; 7819 MW; 687638661E98DEE0 CRC64;
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Last annotation update)
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STRAIN=NEW ZEALAND WHITE; TISSUE=Skeletal muscle;
MEDLINE=98191144; PubMed=9530113;
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Vascular endothelial growth factor (Fragment)
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ProDom; PD001629; PD_growth_factor; 1.
SMART; SM00141; PDGF; 1.
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                                                                                                                                                                                                                                                                                             Capreolus capreolus (Roe deer).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Cervoidea,
Cervidae, Odocoileinae, Capreolus.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Capra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wagener A., Blottner S., Goritz F., Fickel J.; "Detection of growth factors in the testis of roe deer (Capreolus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
                                                                             01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0UN-2003 (TrEMBLrel. 24, Last annotation update)
Vascular endothelial growth factor isoform 121 (Fragment).
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GO; GO:0008083; F:growth factor activity; IEA.
GO; GO:0008151; F:cell growth and/or maintenance; IEA.
InterPro; IPR002400; GF_cysknot.
InterPro; IPR000072; PD_growth_factor.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Vascular endothelila growth factor 165 (Fragment).
Capra hircus (Goat).
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ProDom; PD001629; PD growth_factor; 1.
SMART; SM00141; PDGF, 1.
PROSITE; PS00249; PDGF 1; 1.
PROSITE; PS50278; PDGF 2; 1.
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MEDLINE=20532861; Pubmed=11078967;
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EMBL; AF152593; AAF73232.1; -.
HSSP; P49763; 1FZV.
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TISSUE=Corpus luteum;
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Clausen I., Kietz S., Fischer B.;

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Clausen I., Kietz S., Fischer B.;

Clausen I., Kietz S., Fischer B.;

Transcriptional changes in rabbit preimplantation blastocysts upon exposure to polychlorinated biphenyls.";

Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.

REMEL, AM405795; AA404218.1;

CO, GO:0008083; F:growth factor activity; IEA.

GO, GO:000819; P:growth factor activity; IEA.

GO, GO:000819; P:growth factor.

R DO, GO:000819; P:growth factor.

R InterPro; IPR00040; GF cysknot.

R PROMY; PR00441; PDGF; I.

R PROMY; PR00441; PDGF; I.

R PRODM; PD001629; PD growth factor; I.

R PRODM; PD01629; PD growth factor; I.

R PROSTIE; PS00249; PDGF I; I.

R PROSTIE; PS00249; PDGF I; I.

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R PROSTIE; PS00249; PDGF I; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Capreolus capreolus (Roe deer).
Bukaryota, Metazoa, Chordate, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butharia, Cetartiodactyla, Ruminantia, Pecora, Cervoidea,
Cervidae, Odocoileinae, Capreolus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.8%; Score 45; DB 6; Length 120; 77.8%; Pred. No. 0.33; Live 1; Mismatches 1; Indels
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1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
vascular endothelial growth factor isoform 165 (Fragment).
Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
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GO; GO:0008083; F:growth factor activity; IEA.
GO; GO:0008081; P:cell growth and/or maintenance; IEA.
InterPro; IPR002400; GF cysknot.
InterPro; IPR000072; PD_growth_factor.
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PRINTS; PR00438; GFCYSKNOT.
ProDom; PD001438; GFCYSKNOT.
SMART; SM00141; PDGF; 1.
PROSITE; PS00249; PDGF 1; 1.
PROSITE; PS50278; PDGF 2; 1.
NON_TER 123 123
SEQUENCE 123 AA; 14354 MW; 0A756F541.
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MEDLINE=20532861; PubMed=11078967;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anim. Reprod. Sci. 64:65-75(2000).
EMBL; AF152594; AAF73233.1; -.
HSSP; P49763; 1FZV.
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TISSUB-Placental artery endothelium;
Zheng J., Tsoi S.C., Magness R.R.;
"Growth factor expression in ovine fetal placental artery endothelial
                                                                                                                                                                                                                                                                                                     Gaps
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Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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                                                                                                                                                                                                                             Score 45; DB 6; Length 109;
Pred. No. 0.3;
1; Mismatches 1; Indels
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
BMBL; AP250375; AAF75258.1; -.
HSSP; P49763; 1F2V.
                                                                                                                                    NON TER 1 1 1 SEQUENCE 109 AA; 12656 MW; 912657251A37E023 CRC64;
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GO; GO: 0008083; F:growth factor activity; IEA.
GO; GO: 0008151; P:cell growth and/or maintenance; IEA.
InterPro; IPR002400; GF_cysknot.
PREAP. IPR000072; PD_growth_factor.
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01-UIN-2003 (TrEMBLrel. 24, Created)
01-UIN-2003 (TrEMBLrel. 24, Last sequence update)
01-007-2003 (TrEMBLrel. 25, Last annotation update)
Vascular endothelial growth factor (Fragment)
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Vascular endothelial growth factor (Fragment)
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ProDom; PD001629; PD growth factor; 1.
SMART; SM00141; PDGF; 1.
      Pfam, PF00341; PDGF; 1.
ProDom; PD001629; PD growth factor; 1.
SMART; SM00141; PDGF; 1.
PROSITE; PS50278; PDGF_2; 1.
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                                                                                                                                                                                                                                   Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative
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57 CCNDESLEC 65
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PROSITE; PS00249; PDGF 1; 1. PROSITE; PS50278; PDGF 2; 1.
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                                 SEQUENCE FROM N.A.
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                                                                                               PubMed=12692275;
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Augustin H.G., Ziche M., Lanz C., Buettner M., Rziha H.J., Dehio C.,
"A novel vascular endothelial growth factor encoded by orf virus,
VEGF-E, mediates angiogenesis via signalling through VEGFR-2 (KDR) but
not VEGFR-1 (FIL-1) receptor tyrosine kinases.";
                                    Gaps
                                                                                                                                                                                                                                                                                                                                            01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 24, Last amnotation update)
Vascular endothelial growth factor-3 (Fragment).
Capreolus capreolus (Roe deer).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia; Pecora, Cervoidea;
Cervidae; Odocolleinae, Capreolus.
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A Wagener A., Fickel J.;

Ragener A., Fickel J.;

Nagener A., Fickel J.;

Loudited (MAY-202) to the EMBL/GenBank/DDBJ databases.

EMBL; AF514284; AAM9789.1; --

GO; GO:0016020; C:membrane; IEA.

R GO; GO:0008151; P:cell growth factor activity; IEA.

R GO; GO:0008151; P:cell growth and/or maintenance; IEA.

R InterPro; IPR000072; PD_growth_factor.

R Pfam; PF00341; PDGF; 1.

R Probom; PD001629; PD_growth_factor.

R Probom; PD01629; PD_growth_factor.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Vascular endothelial growth factor homolog Vegf-e (Vascular endothelial growth factor-like protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.8%; Score 45; DB 6; Length 131; 77.8%; Pred. No. 0.36; ive 1; Mismatches 1; Indels
                                 1; Indels
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77.8%; Pred. No. 0.34;
                                                                                                                                                                                                                                                                                                    131 AA.
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                              1; Mismatches
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MEDLINE=99107753; PubMed=9889193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50278; PDGF_2; 1.
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Best Local Similarity 77.00,
1, Conservative
                        7; Conservative
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|CCNDESLEC 32
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Best Local Similarity
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NCBI_TaxID=10258;
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SEQUENCE
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Rziha H.-J., Bauer B., Adam K.-H., Rottgen M., Cottone R., Henkel M., Dehio C., Buttner M.; "Relatedness and heterogeneity at the near-terminal end of the genome of a parapoxvirus bovis 1 strain (B177) compared with parapoxvirus ovis (Orf virus).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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MCIDIBE C.J., Wood A.R.;
MCIDIBE C.J., Wood A.R.;
MCIDIBE C.J., Wood A.R.;
MCIDIBE C.J., Wood A.R.;
MCIDIBE C.J., Wood A.R.;
MCIDIBE C.J., Wood A.R.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
SUBMIL, A7236150; AAP03726.1;
GO; GO:0016020; C:membrane; IEA.
GO; GO:0008151; P:cell growth and/or maintenance; IEA.
InterPro; IPR000072; PD_growth_factor.
InterPro; IPR000072; PD_growth_factor.
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81.8%; Score 45; DB 12; Length 136;
Best Local Similarity 77.8%; Pred. No. 0.37;
Matches 7; Conservative 1; Mismatches 1; Indels
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SMART; SM00141; PDGF: 1.
PROSITE; PS00249; PDGF 1; 1.
PROSITE; PS00278; PDGF 2; 1.
SEQUENCE 132 AA; 14763 MW; 15F403A068B72926 CRC64;
                                                                                                                                                                                                                                                   GO; GO:0016020; C:membrane; IEA.
GO; GO:0008083; F:growth factor activity; IEA.
GO; GO:0008151; P:cell growth and/or maintenance; IEA.
InterPro; IPR002400; GF_cysknot.
InterPro; IPR000072; PD_growth_factor.
Pfam; PF00341; PDGF; 1.
PRINTS; PR00438; GFCYSKNOT.
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136 AA; 15082 MW; 9768C9C42E6CB267 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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PRINTS, PR00438; GFCYSKNOT.
ProDom; PD01629; PD growth_factor; 1.
SMART; SM00141; PDGF; 1.
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                                                                                                                                          J. Gen. Virol. 84:1111-1116 (2003)
BMBL; AR106020; AAD03735.1; --
EMBL; AX16673; AAO31702.1; --
HSSP; P49763; 1FZV.
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70 CCNDESLEC 78

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                                                                                                                        Xenopus laevis (African clawed frog).

Menopus, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Amphibia; Batrachia, Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae, Xenopus.
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SEQUENCE FROM N.A.

A CLEASAR O., Tonissen K.F., Saha M.S., Krieg P.A.;

A CLEASAR O., Tonissen K.F., Saha M.S., Krieg P.A.;

"Neovascularization of the Xenopus embryo.";

Dev. Dyn. 0:0-0(1997).

REMBL, AFO08593; AAB63679.1; -.

REMBL, AFO08593; AAB63679.1; -.

REMBL, AFO08593; F:growth factor activity; IEA.

GO; GO:0008083; F:growth factor activity; IEA.

GO; GO:0008151; P:cell growth and/or maintenance; IEA.

RO; GO:0008151; P:cell growth factor.

InterPro; IFR000072; PD_growth_factor.

RICHERTO; IFR00141; PGFF; 1.

REMINTS: PR00414; PGFF; 1.

REMINTS: PR00414; PGFF; 1.

REMINTS: PR00414; PGFF; 1.

REMINTS: PR00414; PGFF; 1.

REMINTS: PR00414; PGFF; 1.

REMINTS: PS00248; PGFF; 1.

REMINTS: PS00248; PGFF; 1.

REMINTS: PS00248; PGFF; 1.
                                                                 01-07N-1998 (TrEMBLrel. 05, Created)
01-07NN-1998 (TrEMBLrel. 05, Last sequence update)
01-0JUN-2003 (TrEMBLrel. 24, Last annotation update)
Vascular endothelial growth factor 122.
                                     148 AA
                                     PRT;
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Best Local Similarity 77.8
Matches 7; Conservative
                                     PRELIMINARY;
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Search completed: September 5, 2004, 09:59:59 Job time: 21.3636 secs

86 CCNDESLEC 94

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9; Search time 29.5455 Seconds (without alignments) 86.068 Million cell updates/sec
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version 5.1.6 - 2004 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
GenCore 1
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                                                                                                                                                    Title:
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Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing:

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* A_Geneseq_29Jan04:* 1: geneseqp1980s:* 2: geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	u04528	Aau04522 Human VEG	Aau04520 Human VEG	Aay23889 Human vas	н	Abb84621 Human wil	Abg73779 Human NVR	Aaw53240 Homo sapi	Aay97572 Human VEG	Aaw44293 Human vas	Aaw49036 Human zve	н	Aab10649 Human VEG	Aay70750 Human pre	Human	Aab29049 Human VEG	Aab37606 Human VEG	Aay97573 Human VEG	Aau08441 Polypepti		G	Abb84623 Human VEG	Add08950 Human VEG	Aau04552 VEGF base	Abg73750 Human VEG
SUMMARIES	ID	AU04	AAU04522	AAU04520	AAY23889	AAB11931	ABB84621	ABG73779	AAW53240	AAY97572	AAW44293	AAW49036	AAW53241	AAB10649	AAY70750	AAY70983	AAB29049	AAB37606	AAY97573	AAU08441	ABG33055	ABG32046	ABB84623	ADD08950	AAU04552	ABG73750
	DB		4	4	~	m	9	9	7	4	7	7	~	m	m	ო	m	4	4	4	Ŋ	S	9	7	4	9
	Length	6	73	96	109	109	109	287	325	325	354	354	354	354	354	354	354	354	354	354	354	354	354	354	σ	109
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Aau04553 VEGF base	Aaw44296 Rat vascu	Aab70685 Human vas	Aaw14994 Human c-F	Aau04525 VEGF base	Aaw86229 Poxvirus	Aaw86228 Poxvirus	Aam47933 Mouse VEG	Aaw86227 Poxvirus	Aaw86226 Poxvirus	Aar10916 Bovine va	Aar38916 Bovine VE	Aaw40305 Parapox v	Aay33434 Parapox v	Aay92776 Orf virus	Aay97574 Human VEG	Aau08466 Polypepti	Aay33443 Parapox v	Aay33435 Parapox v	Aaw86206 Poxvirus
AAU04553	AAW44296	AAB70685	AAW14994	AAU04525	AAW86229	AAW86228	AAM47933	AAW86227	AAW86226	AAR10916	AAR38916	AAW40305	AAY33434	AAY92776	AAY97574	AAU08466	AAY33443	AAY33435	AAW86206
4	2	4	2		7			7	2	•	2	2	2	3	4	•	•	2	7
uì	326	354	620	80	101	106	110	111	116	120	120	132	132	132	132	132	133	133	133
89.1	89.1	87.3	87.3	83.6	81.8	81.8	81.8	81.8	81.8	81.8	81.8	81.8	81.8	81.8	81.8	81.8	81.8	81.8	81.8
49	49	48	48	46	45	45	45	45	45	45	4.5	45	45	45	45	45	45	45	45
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

residue 1 of an identical peptide to form a dimeric peptide, or between residue 1 and residue 17 of the sequence appearing as AAU04527 also forming a dimeric peptide." /note= "A disulfide bond forms between residue 1 and Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic. 9.
 7. This bond cyclises the peptide" VEGF based bicyclic dimeric peptide #2. Location/Qualifiers 1 AAU04528 standard; protein; 9 AA entry) (first Key Disulfide-bond WO200152875-A1. Disulfide-bond 26-SEP-2001 Synthetic. AAU04528; RESULT 1 AAU04528 

Cendron A; Stacker S, (LUDW-) LUDWIG INST CANCER RES. 18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P. 18-JAN-2001; 2001WO-US001533 Achen MG, Hughes RA, 26-JUL-2001

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.

WPI; 2001-442248/47.

Claim 59; Page 32; 102pp; English.

whose 3-dimensional structure is modelled on the expose loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomerric monocyclic peptide by a measuring beta-beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidiasing the expision and exposed loop of a growth factor protein and cyclising the peptide by oxidiasing the peptide with at least one amino acid deleted prior peptides, dimeric bicyclic peptides (Comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior cyclisation are used to interfere with anglogenesis, necessaries and anglogenesis in a mammal with a condition characterised by anglogenesis, necessaries and paper or condition is diabetic retinopathy, psoriasis, arthropathy, cerebrovascular accident, post-angloplasty restencis, head, heat or corresponding, vascularised necessaries are also used to modulate vascular permeability in a mammal (the mammal has a condition of the liver, excessive corpusion. The peptides are also used to modulate vascular permeability in accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic corpusion in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic corpusion in peripheral activity induced by VEGF. VEGF-C or D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation with an anti-inflammatory agent, to treat a chronic inflammation with an anti-inflammatory agent, to treat a chronic inflammation with an anti-inflammatory agent, to treat a chronic inflament. The sequence represents a dimeric bicyclic peptide of the invention, Human; VEGF-D; vascular endothelial growth factor; angiogenesis; .; 0 neovascularisation, lymphanglogenesis, psoriasis, tumour, diabetes induced neovascular sequelae, rheumatoid arthritis, diabetic retinopathy, chronic inflammation. Cendron A; Human VEGF-D amino acids Val101-Thr 173. AAU04522 standard; protein; 73 AA. Stacker S, (LUDW-) LUDWIG INST CANCER RES. 18-JAN-2001; 2001WO-US001533. 18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P. 26-SEP-2001 (first entry) Conservative Achen MG, Hughes RA, 1 CCNEESLIC 9 Query Match Best Local Similarity '-hea 9; Conserve 1 CCNEESLIC 9 diabetic retinopathy WPI; 2001-442248/47. WO200152875-A1. Sequence 9 AA; Homo sapiens 26-JUL-2001. AAU04522; RESULT 2 AAU04522 g ò

Novel monomeric monocyclic peptide, used to interfere with angiogenesis,

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Gaps

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The sequence represents Human VEGF-D (vascular endothelial growth factor)

amino acids Val101-Thr 173, used together with the C-terminal 23 residues

CC of VEGF to make a hybrid theoretical molecule for 3 dimensional

condelling. The sequence is used in a method of producing a monomeric

modelling. The sequence is used in a method of producing a monomeric

con opposite antipazallel strands of a peptide loop fragment from an

exposed loop of a growth factor protein and cyclising the peptide by

coxidising the cysteine residues. The monocyclic peptides, dimeric

coxidising the cysteine residues. The monocyclic peptides dimeric

coxidising the cysteine residues. The monocyclic peptides of a cyclic

cc betyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic

coxidising the cysteine residues. The monocyclic peptides by

coxidising the cysteine residues. The monocyclic peptides by

coxidising the cysteine residues in remained a link a condition or characterised by

completed with at least one amino acid deleted prior to cyclisation are

coxidising the cysteine residues; newsecularisation or

coxidising the cysteinesis, arthropathy, hemangiomer. The condition is

diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised

coxidition to repend to model the liver, excessive hormone-related angiogenic

condition characterised induced neovascular sequelae, hypertension induced

condition characterised by fluid accumulation. The peptides are also

condition characterised by fluid accumulation in peripheral limbs or in

clungs, peritoneal cavity, pleura, or brain. The peptides are used to

inage blood vessels and lymphatic vasculature. The monomeric and bicyclic

inage blood vessels and lymphatic vasculature. The monomeric and bicyclic

induced by VEGF-C or -D and are also used in combination with an

cultiliammatory agent, to treat a chronic inflammation, especially year

condition arthritis, psoriasis and diabetic retinopathy
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or lymphangiogenesis, is produced by cyclizing a peptide loop fragment trom an exposed loop of a growth factor protein by oxidizing the cysteine residues.
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neovascularisation; lymphangiogenesis; psoriasis; tumour;
diabetes induced neovascular sequelae; rheumatoid arthritis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 55; DB 4; Length 73; 100.0%; Pred. No. 0.44; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diabetic retinopathy; chronic inflammation
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                                                                                             Example 1; Page 90-91; 102pp; English.
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 73 AA;
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  HHHXXXXX
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The sequence represents Human VEGF-D (vascular endothelial growth factor)

amino acids Val101-PRO186. The sequence is used in a method of producing
ca monomorpic monocyclic peptide by a measuring beta-beta carbon separation
distances on opposite antiparallel strands of a peptide loop fragment
from an exposed loop of a growth factor protein and cyclishing the peptide
conversation of proteine residues. The monocyclic peptides, dimeric
bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic
peptide with at least one amino acid deleted prior to cyclisation are
used to interfere with angiogenesis, neovascularisation or lymphangiogenesis. The condition is
used to interfere with angiogenesis, neovascularisation or lymphangiogenesis. The condition is
diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised
angioplasty restenosis, head, heat or cold trauma, substance-induced
neovascularisation of the liver, excessive hormone-related angiogenic
dysfunction, diabetes induced neovascular sequelae, hypertension induced
neovascular sequelae, or chronic liver infection. The peptides are also
used to modulate vascular permeability in a mammal (the mammal has a
condition characterised by fluid accumulation in peripheral limbs or in
lungs, peritoneal cavity, pleura, or brain. The peptides are used to
image blood vessels and lymphatic vasculature. The monomeric and bicyclic
peptides are used to interfere with at least one biological activity
articles are used to interfere with at least one biological activity
articles are used to interfere with at least one biological activity
articles articles and lymphatic vasculature. The monomeric and bicytles articles and interfere with at least one biological activity articles articles and interfere with a least one biological activity articles.
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                                                                                      Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy
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  Cendron A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                    Example 1; Page 89; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY23889 standard; protein; 109 AA.
  Stacker S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Conservative
  Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    σ
                                            WPI; 2001-442248/47
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  Achen MG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                     residues
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The present sequence represents human vascular endothelial growth factor (VGGF)-D. The specification describes a human cell line which stably expresses VEGF-D, or fragments/analogues having VEGF-D biological activity. VEGF-D antagonists, e.g. antisense nucleic acids or triplex useful for the treatment or alleviation of malignant melanomas, tumnours or psoriasis. Angiogenesis and lymphangiogenesis stimulating amounts of VEGF-D can be administered to enhance the acceptance and/or healing of skin grafts or to stimulate the healing of a surgical or traumatic wound to the skin. Lymphangiogenesis stimulating amounts of votes I ymphedema. Endothelial proliferation stimulating amounts of VEGF-D are used to treat antibodice act scleroderma. Vascularisation stimulating amounts of verse be used to treat antibodice ctodermal dysplasia. VEGF-D antibodies are useful for detecting tumours expressing VEGF-D. Pully-crocessed VEGF-D can be used to stimulating amounts of successed VEGF-D can be used to stimulate at least one vEGF-D incoactivity chosen from endothelial cell proliferation, migration, survival and differentiation and lymphangiogenesis without inducing vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                          A human cell line stably expressing vascular endothelial growth factor D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         monoclonal antibody; VEGF receptor; VEGFR-2; VEGFR-3; vascular permeability disorder; endothelial cell proliferative disorder; anglogenic disorder; propriet disorder; neovascularisation disorder; endothelial cell differentiation disorder; cancer; diabetic retinopathy; psoriasis; arthropathy; pulmonary oedema; detection; diagnosis; imaging; lymphatic vasculature.
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Similarity 100.0%; Pred. No. 0.63;
9; Conservative 0; Mismarcher
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                                                                                                                               useful for treating melanomas or tumors expressing VEGF-D.
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                                    Alitalo K;
                                                                                                                                                                  Claim 6; Page 72; 79pp; English.
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(LUDW-) LUDWIG INST CANCER RES.
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99US-0134556P.
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                                    Achen MG, Stacker SA,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 109 AA;
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17-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Achen MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
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08-APR-2002; 2002WO-DK000233

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                                                 Novel compositions comprising antibodies reactive to vascular endothelial growth factor-D, useful for treating, e.g. angiogenesis, lymphogiogenesis and neovascularization disorders.
                                                                                                                                                                           (vascular endothelial growth factor D), lacking both the N- and C-terminal regions. The invention relates to a monoclonal antibody, or fragments thereof, which is specifically reactive with the truncated human VEGF-D, and methods of preparing the antibody. The antibody of the invention interferes with the binding of VEGF-D to the VEGF receptors VEGFR-2 and VEGFR-3, but does not interfere with the binding of VEGF to these receptors and additionally is not reactive with VEGF.C. The antibody may be used to treat disorders associated with vascular permeability, endothelial cell proliferation, angiogenesis, lymphangiogenesis, neovascularisation and endothelial cell differentiation, especially cancer, diabetic retinopathy, psoriasis, and arthropathies. The antibody may also be used to treat fluid accumulation in the heart and/or lung via medulation of vascular permeability. It may additionally be used to detect VEGF-D and may be used to image lymphatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; single-chain; extracellular ligand-binding domain; VBGF;
vascular endothelial growth factor; VBGF type 2 receptor; KDR; Flt-4;
VBGF type 3 receptor; VBGF-C; VBGF-D; signal transduction; angiogenesis;
lymphanglogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as Gln in Claim 9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8. .18
hote= "region of monomer likely to be modified by
mutation as described in claim 9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70. .86
/note= "region of monomer likely to be modified by
mutation as described in claim 9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "region of monomer likely to be modified by mutation as described in claim 9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "region of monomer likely to be modified by mutation as described in claim 9"
                                                                                                                                                              This sequence represents a 109 amino acid truncated human VEGF-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 55; DB 3; Length 109; 100.0%; Pred. No. 0.63; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "This residues is described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human wild-type VEGF-D monomer SEQ ID 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB84621 standard; protein; 109 AA.
                                                                                                                           Claim 1; Fig 1; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         vasculature in tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CCNEESLIC 9
               WPI; 2000-442498/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 CCNEESLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200281520-A2
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Region
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Matches
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This invention describes a novel single-chain dimeric polypeptide which binds to extracellular ligand-binding domain of vascular endothelial growth factor (VEGF) type 2 receptor (KDR) or VEGF type 3 receptor (FIL-4). The polypeptide of the invention comprises two receptor-binding sites of which one is capable of binding to a ligand-binding domain of the receptor, and at least one monomer of the dimeric comain of the receptor, and at least one monomer of the dimeric polypeptide is derived from VEGF. Or VEGF-C or VEGF-D, where the polypeptide of scapable of binding to the receptor, but incapable of activating the receptor. The polypeptide of the invention is useful for preparing a medicament for preventing or treating a disease or condition involving increased signal transduction from, or an increased activation of a VEGF or type 3 receptor e.g. for inhibiting angiogenesis or I will be additioned and used in the construction of a VEGF-D monomer which can be modified and used in the construction of a VEGF-D and KDR antagonist described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                Novel single-chain dimeric polypeptide for inhibiting angiogenesis, binds to extracellular ligand-binding domain of vascular endothelial growth factor type 2/type 3 receptor but does not activate the receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /nore= "Encoded by TAA, an in frame stop codon which interrupts the coding region as shown in Figure 1A-B. This site is the end of the protein sequence represented in SEQ ID 1 of the Sequence listing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NVR; human; endothelial growth factor; cytostatic; cancer; angiogenesis; cell proliferation; revascularisation; amputation; vasculogenesis; transplant; brain; breast; intestine; kidney; lung; ovary; pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "Region not represented in SEQ ID 1 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 55; DB 6; Length 109; 100.0%; Pred. No. 0.63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG73779 standard; protein; 287 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence listing"
                                                                                                                                                                                                                                                                                               Claim 9; Page 66; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prostate; uterus; gene therapy
                                                  06-APR-2001; 2001DK-0000578.
06-APR-2001; 2001US-0282239P.
                                                                                                        (MAXY-) MAXYGEN HOLDINGS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                            Boesen TP, Halkier T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 CCNEESLIC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CCNEESLIC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
'Loca 9; Conserve
                                                                                                                                                                                 WPI; 2003-058505/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human NVR protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 109 AA;
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Claim 16; Page 57-58; 101pp; English
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UNIV HELSINKI LICENSING LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human VEGF-D protein sequence.
                                                                                                                                                            97AU-00004954.
97US-0038814P.
97AU-00007435.
                                                                                     97WO-US014696
                                                                                                            96AU-00001825.
                                                                                                                                    96AU-00003554
96US-0031097P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 CCNEESLIC 124
                                                                                                                                                                                                                                                           Achen MG, Wilks AF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CCNEESLIC 9
                                                                                                                                                                                                                                                                                 WPI; 1998-179057/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 9; Conserv
                                                                                                                                                                                                                                                                                               N-PSDB; AAV20806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 325 AA;
                                     W09807832-A1
                                                                                     21-AUG-1997;
                                                            26-FEB-1998
                                                                                                                          23-AUG-1996
11-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-APR-2001
                                                                                                             23-AUG-1996
                                                                                                                                                 14-NOV-1996
                                                                                                                                                                         10-FEB-1997
                                                                                                                                                                                               01-JUL-1997
                                                                                                                                                             05-FEB-1997
                                                                                                                                                                                    19-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                       (LUDW-)
                                                                                                                                                                                                                                    (UYHE-)
      Region
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Matches
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ID AAY9
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                                                                                                                                                                                                                                                  This invention describes a novel human endothelial growth factor polypeptide which has cytostatic activity. The polypeptide and its encoding polymotleotide are useful in the diagnosis, prevention, and treatment of cancer and other conditions or diseases involving angiogenesis and cell proliferation. NVR may also be used to promote reconstruction or added to a tissue culture to promote vasculagenesis in tissues for autologous or heterologous transplant. Antagonists or inhibitors of NVR may be used to suppress or prevent angiogenesis and thus prevent the growth and development of cancers such as cancer of the brain, breast, intestine, kidney, lung, ovary, pancreas, prostate or uterus. The products of the invention can be used for gene therapy. This sequence represents the human NVR protein described in the disclosure of
                                                                                                                                                                                New endothelial growth factor polypeptide and polynucleotides, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vascular endothelial growth factor; VEGF-D; angiogenesis; modification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diabetic retinopathy; lung disorders; blood circulation; gaseous exchange; chronic obstructive airway disease; intestinal malabsorptive syndrome; biopsy; metastatic risk; detection; diagnosis; congestive heart failure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                             diagnosing, preventing, and treating cancer and other conditions or diseases involving angiogenesis and cell proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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156. .158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "potential N-linked glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Length 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens vascular endothelial growth factor D (VEGF-D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acceleration; wound healing; tissue; organ; transplants; collateral circulation; infarction; arterial stenosis; coronary artery disease; inhibition; cancer; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 55; DB 6 100.0%; Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW53240 standard; protein; 325 AA
                                                                                                                                                                                                                              Claim 1; Fig 1A-B; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .,
                                                                                                                       Murry LE;
                                              09-JAN-2002; 2002US-00044622.
                                                                     97US-00788812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                             (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 CCNEESLIC 153
                                                                                                                     Goli SK,
                                                                                                                                             WPI; 2003-182635/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CCNEESLIC
                                                                                                                                                         N-PSDB; ABQ77105
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 287 AA;
US2002155538-A1
                                                                                                                                                                                                                                                                                                                                                                                                                 invention
                                                                      23-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                       24-OCT-2002
                                                                                                                      Bandman O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW53240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
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The sequence is that of human breast vascular endothelial growth factor D (VBGF-D). VBGF-D can be used for e.g. acceleration of angiogenesis in wound healing, tissue or organ transplantation, or to establish collateral circulation in tissue infarction or arterial stenosis, such as coronary artery disease, and inhibition of angiogenesis in the treatment treatment of cancer or of diabetic retinopathy. It can also be used in the treatment treatment of lung disorders to improve blood circulation in the lung and/or gaseous exchange between the lungs and the blood stream or to improve blood circulation to the heart and 02 gas permeability in cases of cardiac insufficiency, to improve blood flow and gaseous exchange in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chronic obstructive airway disease, or to treat malabsorptive syndromes in the intestinal tract. Quantitation of VBGF-D in cancer biopsy specimens may be useful as an indicator of titure metastatic risk. Antagonists can be used for treating e.g. conditions such as congestive heart failure, involving accumulations of fluid in the lung resulting from increases in vascular permeability. The products can also be used for detection and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated vascular endothelial growth factor-D - used to develop products for use in e.g. modifying angiogenesis or treating lung, heart or intestinal disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; angiogenic protein; wound healing; vascular tissue repair;
peripheral arterial disease; critical limb ischaemia; coronary disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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258. .260
/note= "potential N-linked glycosylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Human; vascular endothelial growth factor D; VEGF-D; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human zvegf2 growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 CCNEESLIC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CCNEESLIC 9
                                        inflammation; oedema
                                                                                                                                                                                                                                                                                                                                WPI; 1998-110591/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the VEGF-D protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                              Hirata Y, Nezu J;
                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAV15156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 354 AA;
                                                                                                                                                                                                                                                                                                                                                                                                        treating oedema.
                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Binding-site
                                                                                                                                                                                                                       15-JUL-1996;
                                                                                                            WO9802543-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-OCT-1998
                                                                                                                                                22-JAN-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW49036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
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AAW49036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence is vascular endothelial growth factor-D (VEGF-D), which is an angiogenic protein of the invention. The angiogenic proteins and the DNA sequences encoding them, are used to prevent, treat or ameliorate disease and to detect diseases, or susceptibility, by detecting mutations or the presence or amount of angiogenic protein expression. Particularly citssue, and for repair of vascular tissue, especially peripheral arterial disease, critical limb ischaemia or coronary disease. Antagonists of the sequences are used to inhibit angiogenesis in tumours and to treat inflammation (where associated with increased vascular permeability), diabetic retinopathy, rheumatoid arthritis or psociasis. Agonists are also used to identify specific binding agents (potential therapeutic agents) cand to raise antibodies. The antibodies are useful as therapeutic agents) cand to raise antibodies. The antibodies are useful as therapeutic cand to raise antibodies. The antibodies are useful as therapeutic continuing when linked to e.g. a label or cytocial, and for in vivo or in vitro diagnosis (including imaging) or for therapy continuing when linked to e.g. a label or cytocial, and for the immunotyping of cells, e.g. for detecting minimal residual disease or immunotyping of cells, e.g. for detecting minimal residual diseases continually bacterial, fungal or parasitic); neurodegeneration, also as chemotactic agents or for treating regeneration of the nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding angiogenic proteins, useful e.g. for promoting healing of wounds and treating peripheral arterial disease, critical limb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
angiogenesis; tumour; inflammation; diabetic retinopathy; psoriasis; rhemmatoid arthritis; autoimmume disease; allergy; cancer; therapy; infectious disease; neurodegeneration; vascular endothelial growth factor-D; VEGF-D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 55; DB 4; Length 325; 100.0%; Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human vascular endothelial growth factor D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Page 226-227; 244pp; English.
                                                                                                                                                                                                                                                                                                                 Cao L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW44293 standard; protein; 354 AA.
                                                                                                                                                                                                      01-JUN-2000; 2000WO-US014925.
                                                                                                                                                                                                                                          99US-0137796P.
                                                                                                                                                                                                                                                                                                                                                                                                                                             ischemia or coronary disease.
                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                               Hu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.v.
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 CCNEESLIC 124
                                                                                                                                                                                                                                                                                                               Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-071057/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CCNEESLIC
                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAA91006.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 325. AA;
                                                                                                                               WO200075163-A1.
                                                                                                                                                                                                                                          03-JUN-1999;
                                                                                               Homo sapiens
                                                                                                                                                                    14-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW44293;
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The present sequence represents human vascular endothelial growth factor D (VEGF-D). The VEGF-D protein, compounds and antibodies, which can bind the protein, may be useful in, e.g. gene therapy and in treatment of inflammation and oedema. Vectors, containing the VEGF-D DNA, and VEGF-D DNA sequences may be used for screening for the compounds which bind to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human zvegf2 growth factor; mitogen; fibroblast; smooth muscle cell; venous stasis ulcer; diabetic ulcer; skin wound; chemotactic effect; angiogenic effect; tumour; diabetic retinopathy; psoriasis; arthritis; scleroderma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                 VEGF-D protein encoded by DNA - useful for, e.g. gene therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 55; DB 2; Length 354; 100.0%; Pred. No. 1.8;
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                                                        (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Cysteine-rich domain"
257. .274
/note= "Balbiani ring motif"
275. .294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .. .23
'note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 18-20; 52pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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109. .197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW49036 Btandard; protein; 354 AA.
96JP-00185216.
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Region

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The sequence is that of human lung vascular endothelial growth factor D (VEGF-D). VEGF-D can be used for e.g. acceleration of angiogenesis in wound healing, tissue or organ transplantation, or to establish collateral circulation in tissue infarction or arterial stenosis such as coronary artery disease, and inhibition of angiogenesis in the treatment of cancer or of diabetic retinopathy. It can also be used in the treatment of lung disorders to improve blood circulation in the lung and/or gaseous exchange between the lungs and the blood stream or to improve blood circulation to the heart and O2 gas permeability in cases of cardiac insufficiency, to improve blood flow and gaseous exchange in chronic obstructive airway disease, or to treat malabsorptive syndromes in the intestinal tract. Quantitation of VEGF-D in cancer biopsy control constructive airway disease, or to treat malabsorptive syndromes in the intestinal tract. Quantitation of VEGF-D in cancer biopsy companies can be used for treating e.g. conditions such as congestive heart failure, involving accumulations of fluid in the lung resulting from it can also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated vascular endothelial growth factor-D - used to develop products for use in e.g. modifying angiogenesis or treating lung, heart or intestinal disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stacker SA, Alitalo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 55; DB 2
Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 16; Page 60-61; 101pp; English
                                                                                                                                                                                                                                                                                                                                                                                                             UNIV HELSINKI LICENSING LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB10649 standard; protein; 354 AA.
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                                                                                                                                                                                                                                                                                                                                                                                     LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                           96US-0031097P.
                                                                                                                                                                         96AU-00001825
96US-0023751P
                                                                                                                                                                                                                   96AU-00003554
                                                                                                                                                                                                                                                                                        97US-0038814P
                                                                                                                             97WO-US014696
                                                                                                                                                                                                                                                                                                                                         97US-0051426P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145 CCNEESLIC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Achen MG, Wilks AF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-179057/16.
N-PSDB; AAV20807.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 354 AA;
                             WO9807832-A1
                                                                                                                          21-AUG-1997;
                                                                                                                                                                                                                                                                                                                                         01-JUL-1997;
                                                                            26-FEB-1998
                                                                                                                                                                       23-AUG-1996;
23-AUG-1996;
                                                                                                                                                                                                                                                                                          LO-FEB-1997;
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                                                                                                                                                                                                                     11-NOV-1996
                                                                                                                                                                                                                                              L4-NOV-1996
                                                                                                                                                                                                                                                                    05-FEB-1997
                                                                                                                                                                                                                                                                                                                   19-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                       (LUDW-)
                                                                                                                                                                                                                                                                                                                                                                                                           (UYHE-)
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Tyegf2 protein in a dimeric form acts as a mitogen for fibroblasts or smooth muscle cells. zvegf2 is claimed to be useful for stimulating the revascularisation of tissue or the re-endochelialisation of vascular classue. Zvefg2 is particularly claimed to be useful for the treatment of till-thickness skin wounds, including venous stasis ulcers and diabetic ulcers. The zvegf2 protein is also claimed to be useful as an additive in tissue adhesives for promoting revascularisation of the healing tissue. The zvegf2 protein is also claimed to be useful as an additive in tissue adhesives for promoting revascularisation of the healing tissue. Chemotactic and angiogenic effects. The antagonists may therefore be useful for reducing growth of solid tumnours by inhibiting the nevascularisation of the developing tumour or by directly blocking tumour cll growth, in the treatment of diabetic retinopathy, psoriasis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated vascular endothelial growth factor - used to develop products for treating e.g. wounds, burns, myocardial infarction, tumours, psoriasis, arthritis, restenosis or organ transplants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vascular endothelial growth factor; VEGF-D; angiogenesis; modification; acceleration; wound healing; tissue; organ; transplants; collateral circulation; infarction; arterial stenoais; coronary artery disease; inhibition; cancer; treatment; diabetic retinopathy; lung disorders; blood circulation; gaseous exchange; chronic obstructive aliway disease; intestinal malabsorptive syndrome; biopsy; metastatic risk; detection; diagnosis; congestive heart failure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                            Nygaard S, Sheppard PO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens vascular endothelial growth factor D (VEGF-D)
                                                 /note= "Cysteine-rich domain""
/note= "Balbiani ring motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 53-54; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW53241 standard; protein; 354 AA.
                                                                                                                                                                                                                                                                                                                                                       Gilbert T, Conklin DC, Hart CE,
                                                                                                                                                                                                                                      96US-00759657
97US-00933455
                                                                                                                                                                                          97WO-US020888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arthritis, and scleroderma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                           295. .354
                                                                                                                                                                                                                                                                                                         (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145 CCNEESLIC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CCNEESLIC 9
                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-333256/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
es 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAV32823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 354 AA;
                                                                                             WO9824811-A2
                                                                                                                                                                                        20-NOV-1997;
                                                                                                                                                                                                                                    06-DEC-1996;
18-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-AUG-1998
                                                                                                                                            11-JUN-1998
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Gaps

0,

AAW53241;

RESULT 12 AAW53241

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Query Match

Matches

Valltola R, Jussila L;

UNIV HELSINKI LICENSING LTD OY.

98US-00169079. 99WO-US023525

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Treating neoplastic diseases such as lymphoma, carcinomas, melanomas and sarcomas, involves administering a compound capable of inhibiting binding of ligand proteins to fms-like tyrosine kinase-1 receptor.
                                                                                                                                                                                                                                                                                                                 Example 15-17; Page 142-143; 148pp; English.
                                                                                                                                         (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                       Alitalo K, Kaipainen A,
                                                                                                                                                                                                                      WPI; 2000-317850/27.
              WO200021560-A1.
                                                                             08-OCT-1999;
                                                                                                            09-OCT-1998;
                                             20-APR-2000.
                                                                                                                                                          (UXHE-)
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has valentary, cytostatic, antirheumatic, antirheumatic, antiproriatic and antidlabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rhewarded arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues regeneration are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair, proliferation of new blood vessels, tissue regeneration and organ repair, proliferation of new blood vessels, issue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents the human VEGD protein used to illustrate the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, receptor tyrosine kinase, RTK; Flt4; fms-like tyrosine kinase 4; VEGFR-3; vascular endothelial growth factor receptor-3; chromosome 5q35; cytostatic; tumour imaging; anti-tumour therapy; treatment; diagnosis; neoplastic disease; lymphoma; carcinoma; breast; squamous cell; melanoma; sarcoma; malignancy; VEGF-D; vascular endothelial growth factor D.
                                                                                                                                                                                                                                                                                                                                                              preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds.
tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
venous sore; diabetic ulcer; burns; skin graft growth; VEGD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                New vascular endothelial growth factor protein, useful for treating
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                                                                                                                                                                                                                                                                    Gosiewska A;
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                                                                                                                                                                                                                                                                   Dijkmans JJH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 11; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY70750 standard; protein; 354 AA.
                                                                                                                                                                                                                                                                    Sprengel JJ, Yon JR,
                                                                                                                                         99WO-US030503.
                                                                                                                                                                                      99US-0124967P.
                                                                                                                                                                        98GB-00028377
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                                                                                                                                                                                                                                     (JANC ) JANSSEN PHARM NV.
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                                                                                                                                                                                                                                                                                                                 WPI; 2000-442669/38.
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Best Local Similarity
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                                                                             WO200037641-A2.
                                                                                                                                                                                                                                                                   Gordon RD, S
Dhanaraj SN,
                                               Homo sapiens
                                                                                                                                         21-DEC-1999;
                                                                                                                                                                        22-DEC-1998;
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                                                                                                                                                                                      18-MAR-1999;
                                                                                                                                                                                                        08-NOV-1999;
                                                                                                            29-JUN-2000
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tissue
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The patent discloses a method to treat neoplastic disease characterised by expression of fms-like tyrosine kinase 4 (Flt4) receptor (also referred as vascular endothelial growth factor receptor-3, vEGFR-3) in endothelial cells of blood vessels adjacent to malignant neoplasm. The endothelial cells of blood vessels adjacent to malignant neoplasm. The rethod involves administering a compound that inhibits binding of a ligand threrby inhibiting Flt4 mediated proliferation of vascular endothelial cells. The compound is useful for treating neoplastic disease such as breast carcinomas, squamous cell carcinomas, lymphomas, melanomas con and sarcomas. Flt4 receptor tyrosine kinase binding compounds can be used for manufacturing medicament useful for diagnostic screening, imaging and treatment of malignancies characterised by Flt4-expressing blood cells.

The Flt4 gene maps to chromosomal region 5q3s and is expressed as 5.8 kb and 4.5 kb mRNAs which differ in their 3' sequences and are cufferentially expressed in HEL and DAMI cell lines. Flt4 belongs to a subfamily of class III receptor tyrosine kinases (FTKS). It is used as a carget for tumour imaging and anti-tumour therapy. The present sequence is a human prepro-vascular endothelial growth factor D (VGF-D), a specific example of Flt4 binding compound. A recombinantly matured VBGF-D lacking residues 1-92 and 202-354 retains the ability to activate VBGFR-2 and VBGFR-3 receptors and associate as non-covalently linked dimers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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100.0%; Pred. No. 1.8;
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22. .92
/label= Amino terminal peptide
/note= "Cleavage results in fully-processed mature VEGF-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present amino acid sequence is the complete human prepro-vascular endothelial growth factor (VEGF)-D. VEGF-D has the ability to stimulate re-endothelialisation of an injured blood vessel, without significant stimulation of smooth muscle cell proliferation. It can bind to and stimulate VEGFR-2 (vascular endothelial growth factor receptor) and/or VEGFR-3 phosphorylation in cells that express such receptors. An antiseteneousis agent comprising either a VEGF-D gene or protein is used in a method to reduce or prevent restenosis and stenosis of a blood vessel following vascular tranma e.g., cardiovascular surgery and percutaneous transluminal coronary angioplasty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Preventing stenosis and restenosis in mammals using vascular endothelial growth factor proteins or the nucleic acids encoding them.
/label= Signal_peptide
/note= "Cleavage results in partially-processed VEGF-D
                                                                                                                                                                          /label= Carboxy terminal peptide
/note= "Cleavage results in partially-processed VEGF-D
                                                                                                             93. .201
/label= Recombinantly_matured VEGF D_protein
/note= "Processed vascular epīthelīaī growth factor-D"
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                                                                                                                                                                                                                                                                                                                                                                     (LUDW-) LUDWIG INST CANCER RES.
(UYHE-) UNIV HELSINKI LICENSING LTD OY.
(YLAH/) YLA-HERTTUALA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 53-55; 61pp; English.
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                                                                                                                                                                                                                                                                                                                                          98US-0105587P,
                                                                                                                                                            .354
                                protein"
                                                                                            protein"
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N-PSDB; AAD00340.
                                                                                                                                                                                                                                            WO200024412-A2
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                                                                                                                                                                                                                                                                            04-MAY-2000.
                                                Peptide
                                                                                                               Protein
                                                                                                                                                              Peptide
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Query Match

100.0%; Score 55; DB 3; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                     145 CCNEESLIC 153
                                                                                       1 CCNEESLIC 9
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Sequence 354 AA;

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Gaps

5, 2004, 09:55:11 Search completed: September Job time: 29.5455 secs

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Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 11, Appl
Sequence 119, Appl
Sequence 6, Appli
Sequence 22, Appli
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                                                                                                     September 5, 2004, 10:00:15; Search time 25.2727 Seconds (without alignments) 112.199 Million cell updates/sec
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Sequence 8,
Sequence 1,
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Sequence 3, A
Sequence 1, A
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(cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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(cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
(cgn2_6/ptodata/2/pubpaa/US008_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-352-153-8
US-10-04-622-1
US-10-274-953-3
US-09-956-005-2
US-09-795-006A-119
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US-09-765-534B-22
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US-09-761-636A-3
US-09-761-636A-1
US-09-956-095-3
                                                                                                                                                                                                                                                                                                          1298764 seqs, 315065143 residues
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                                                                 OM protein - protein search, using sw model
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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## ALIGNMENTS

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RESULT 1

US-09-761-636A-9

i Sequence 9, Application US/09761636A

i Sequence 9. Application US/09761636A

i Retent No. US20020065218A1

i GENERAL INFORMATION:

APPLICANT: STACKEN, Steven

APPLICANT: GENERON, Angela

I TILE CENTRON, Angela

I TILE OF INVENTION: VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR

FILE REFERENCE: 1064/4850S Achen et al

CURRENT FILING DATE: 2001-01-18

PRIOR PLICATION NUMBER: US 60/176,293

PRIOR FILING DATE: 2000-01-18

PRIOR FILING DATE: 2000-01-18

PRIOR FILING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 34

SEQ ID NO 9

LENGTH: 9

LENGTH: 9

CURRENT: Homo sapiens

US-09-761-636A-9

QUETY MAtch

Best Local Similarity 100.0%; Pred. No. 1.2e+06;

MAtches 9; Conservative 0; Mismatches 0; Indels 0; Gaps

OV 1 CCNEESLIC 9

DD 1 CCNEESLIC 9
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; Sequence 3, Application US/09761636A ; Patent No. US20020065218A1

US-09-761-636A-3

RESULT 2

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US20020102260A1
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GENERAL INFORMATION:
APPLICANT: ACHEN, MICHES, Richard
APPLICANT: CENDROM, Angela
TITLE OF INVENTION: VBGF-C/VBGF-C/VBGF PEPTIDOMIMETIC INHIBITOR; FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT FILING DATE: 2001-01-18
PRIOR FILING DATE: 2000-01-18
PRIOR PILING DATE: 2000-01-18
PRIOR PILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 34
NUMBER OF SEQ ID NOS: 34
NUMBER OF SEQ ID NOS: 34
               APPLICANT: ACHEN, Marc
APPLICANT: STACKER, Steven
APPLICANT: HUGHES, Richard
APPLICANT: HUGHES, Richard
APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT FILING DATE: 2000-01-18
PRIOR PLILIATION NUMBER: US 60/176,293
PRIOR PLILING DATE: 2000-01-18
PRIOR PLILING DATE: 2000-01-18
PRIOR PLILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN VERSION 3.0
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NAME/KEY: misc_feature
CTHER INFORMATION: Amino acid residues of Vall01-Pro196 of VEGF-D
US-09-761-636A-1
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NAME/KEY: misc_feature
OTHER INFORMATION: Amino acid residues Vall01-Thr173 of VEGF-D
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Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 55; DB 9; Length 73; 100.0%; Pred. No. 0.2;
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Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: Homo sapiens
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US-09-761-636A-1
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US-09-956-095-3
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LENGTH: 73
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APPLICANT: ACHEN, MACC
TITLE OF INVENTION: EXPRESSION VECTORS AND CELL LINES EXPRESSING VASCULAR
TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR D, AND METHOD OF TREATING
TITLE OF INVENTION: MELANOMAS
FILE REPERENCE: 1064/44385 MAIC ACHEN
CURRENT APPLICATION NUMBER: US/09/219,345A
CURRENT FILING DATE: 1998-12-23
PRIOR PLILING DATE: 1997-12-24
PRIOR PLILING DATE: 1997-12-24
PRIOR PLILING DATE: 1998-05-29
PRIOR FILING DATE: 1998-05-29
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; Publication No. US20040141917A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc G.
; APPLICANT: STACKER, Steve A.
; TITLE OF INVENTION: ANTIBODIES TO TRUNCATED VEGF-D AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 55; DB 9; Length 109; 100.0%; Pred. No. 0.29;
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Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: Homo sapiens
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SOFTWARE: Patentin Vo
SEQ ID NO 1
LENGTH: 109
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Matches 9; Conserv
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IMMEDIATE SOURCE:
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Sequence 8, Application US/10352153
Publication No. US20030211101A1
Sequence 8, Application No. US20030211101A1
Sepulcant: With Mercer, Andrew A
APPLICANT: Wise, Lyn M
APPLICANT: Savory, Loreen J
APPLICANT: Stacker, Stephen B
APPLICANT: Stacker, Stephen B
APPLICANT: Stacker, Stephen B
APPLICANT: Stacker, Stephen B
TITLE OF INVENTION: VASCULAR ENOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF
TITLE OF INVENTION: VASCULAR ENOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF
TITLE OF INVENTION: WEEPPTOR-2, AND USES THEREOF
TITLE OF INVENTION: RECEPTOR-2, AND USES THEREOF
TITLE OF INVENTION: RECEPTOR-2, AND ACTIVATES MANMALIAN VEGF
TITLE OF INVENTION: WEEPPTOR-2, AND 10431, 833
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US/09/431, 888A
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 60/106,689
PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-02
PRIOR APPLICATION NUMBER: EARLIER PILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 11
SSOFTWARE: PATENTIN VET: 2.0
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FILE REFERENCE: ACHEN et al-1064-44660
CURRENT APPLICATION NUMBER: US/10/779,731
PRIOR APPLICATION NUMBER: US/10/100,037
PRIOR FILING DATE: 2002-03-19
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/113,254
PRIOR PRIOR APPLICATION NUMBER: 60/113,254
PRIOR PLING DATE: 1998-12-21
PRIOR PLING DATE: 1998-12-21
PRIOR PLING DATE: 1998-12-21
PRIOR PLING DATE: 1998-12-21
PRIOR PLING DATE: 1998-12-21
PRIOR PLING DATE: 1998-05-17
NUMBER OF SEQ ID NOS: 1
SEQ ID NO 1
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APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.00
Thes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Conservative
                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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Matches 9; Conserv
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US-10-044-622-1
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                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ for Windows Version 2.0
Goli, Surya K.
Murry, Lynn E.
TITLE OF INVENTION: NOVEL ENDOTHELIAL GROWTH
FACTOR
                                                                                         NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATE:

APPLICATION NUMBER: US/10/044,622
FILING DATE: 09-Jan-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 08/788,812
FILING DATE: «Unknown»
APPLICATION NUMBER: 08/788,812
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, LUCY
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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Sequence 3, Application US/10274953

Publication No. US20030114658A1

GENERAL INFORMATION:
APPLICANT: Marc G. ACHEN
APPLICANT: Andrew F. WILKS
APPLICANT: Steven A. STACKER
TITLE OF INVENTION: GROWTH FACTOR
INVBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 280 amino acids
TYPE: amino acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                   ZIP: 94304
COMPUTER READABLE FORM:
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CLONE: 873352
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                      CITY: Palo Alto
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REGISTRATION NUMBER: 26,269
REFERRENCE/DOCKET NUMBER: 1064/42983
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE TYPE: Human Breast
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-161-694-3
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PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09956095
Patent No. US20020102260A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                TELEX: N/A
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
                                                                                                                                                                                                                      TELEFAX: (202) 628-8844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100...
Best Scal Similarity 100...
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Steven A. STACKER
Kari ALITALO
TITLE OF INVENTION: GROWITH FACTOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
STREET: 1200 G Street, NW, Suite 700
CITY: Washington
STATE: DC
CONNECTION: CONNECTION: CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CONNECTION CO
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CURRENT APPLICATION DATA:
APPLICATION NUBER: US/10/161,694
FILING DATE: 05-Jun-2002
CLASSIFICATION: <university control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of t
                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/274,953 FILING DATE: 22-oct-2002
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APPLICATION NUMBER: US/09/296,275
FILING DATE: «Unknown»
PAPLICATION NUMBER: 08/915,795
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/09/296,275
FILING DATE:
APPLICATION NUMBER: 08/915,795
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/42983
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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US-10-161-694-3
; Sequence 3, Application US/10161694
; Publication No. US2003012537A1
; GENERAL INFORMATION:
APPLICANT: Marc G. ACHEN
Andrew P. WILKS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 325 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
TISSUE TYPE: Human Breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: NO
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APPLICANT: ACHEN, MARC G.
APPLICANT: ACHEN, MARC G.
APPLICANT: STACKER, Steven A.
TITLE OF INVENTION: METHODS FOR TREATING NEOPLASTIC DISEASE CHARACTERIZED BY
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR D EXPRESSION, FOR SCREENING
TITLE OF INVENTION: VASCULARIZATION OF TISSUE
TITLE OF INVENTION: VASCULARIZATION OF TISSUE
FILE REFERENCE: 1064/4866667
CURRENT APPLICATION NUMBER: US/09/956,095
CURRENT FILING DATE: 2001-09-20
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GENERAL INFORMATION:
APPLICANT: ACHEN, Marc
TITLE OF INVENTION:
TITLE OF INVENTION: EXPRESSION VECTORS AND CELL LINES EXPRESSING VASCULAR
TITLE OF INVENTION: MEDANOMAS
TITLE OF INVENTION: MELANOMAS
                                                                  Gaps
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100.0%; Score 55; DB 14; Length 325; 100.0%; Pred. No. 0.81;
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Best Local Similarity 100.0%; Pred. No. 0.88;
Batches 9; Conservative 0; Mismatches 0; Indels
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1 CCNEESLIC 9
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Publication No. US20030026759A1
GENERAL INFORMATION:
APPLICANT: Ferrell, Robert E.
APPLICANT: Finegold, David N.
APPLICANT: Finegold, David N.
TITLE OF INVENTION: SCREENING AND THERAPY FOR LYMPHATIC DISORDERS INVOLVING FILE REFERENCE: 28967/352587
TITLE OF INVENTION: SCREENING AND THERAPY FOR LYMPHATIC DISORDERS INVOLVING FILE REFERENCE: 28967/352587
CURRENT APPLICATION NUMBER: US/09/375,248
CURRENT APPLICATION NUMBER: US/09/375,248
SEARLIER APPLICATION NUMBER: PCT/US99/06133
SEARLIER RILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 119, Application US/09795006A

Farent No. US20020151680A1

GENERAL INFORMATION:

APPLICANT: Alitalo et al

FILLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR

TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR

FILLE REFERENCE: 28867/33897/B

CURRENT APPLICATION NUMBER: US/09/795,006A

CURRENT PILING DATE: 2001-02-26

FRIOR PILING DATE: 2000-05-18

FRIOR PILING DATE: 2000-05-18

FRIOR PILING DATE: 2000-05-25

NUMBER OF SEQ ID NOS: 175

SOFTWARE: Patentin Ver. 2.0

LENGTH: 354
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100.0%; Score 55; DB 9; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.88;
Matches 9; Conservative 0; Mismatches 0; Indels
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FILE REFERENCE: 1064/44385 Marc ACHEN
CURRENT APPLICATION NUMBER: US/09/219,345A
CURRENT FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: AU PP 1131
PRIOR FILING DATE: 1997-12-24
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 11
SOCTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 354
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
US-09-219-345A-11
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; ORGANISM: Homo sapiens
US-09-795-006A-119
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US-09-375-248-6
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APPLICANT: Kaipainen, Arja
APPLICANT: Kaipainen, Arja
APPLICANT: Waltola, Reija
APPLICANT: Valtola, Reija
APPLICANT: Useria
APPLICANT: Useria
APPLICANT: Useria
APPLICANT: Useria
APPLICANT: Useria
TITLE OF INVENTION: Flt4 (VEGFR-3) as a Target for Tumor Imaging and Anti-Tumor Thera
FILE REFERENCE: 28113/34891
CURRENT APPLICATION NUMBER: 08/901,710
FRIOR APPLICATION NUMBER: 08/901,710
FRIOR APPLICATION NUMBER: 08/340,011
FRIOR APPLICATION NUMBER: 08/340,011
FRIOR FILING DATE: 1994-11-14
FRIOR FILING DATE: 1994-07-09
FRIOR FILING DATE: 1994-07-09
FRIOR FILING DATE: 1992-10-09
FRIOR FILING DATE: 1992-10-09
FRIOR FILING DATE: 1992-10-09
FRIOR PRICHARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                 100.0%; Score 55; DB 10; Length 354; 100.0%; Pred. No. 0.88; ative 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5, 2004, 10:29:19
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15

9.09-76-554B-22
Sequence 22, Application US/09765534B
Publication No. US20040037820A1
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Kaipainen, Arja
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 354
; TYPE: PRT
; ORCANISM: Homo sapiens
US-09-375-248-6
                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: September
Job time: 26.2727 secs
                                                                                                                                                                                                                                                                                                                                 145 CCNEESLIC 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                     1 CCNEESLIC 9
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Sun Sep

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                  Copyright
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OM protein - protein search, using sw model

Run on:

September 5, 2004, 09:55:30; Search time 8 Seconds (without alignments) 58.079 Million cell updates/sec

US-09-761-636A-9 55 1 CCNEESLIC 9 score: Sequence: Perfect

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

389414 segs, 51625971 residues Searched:

389414 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Issued Patents AA:* Database :

/cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## Re

SUMMARIES	Description	09-469-186-1 Segmenter 1 App.	-469-185-1 Seguence 1.	-888-8 Seguence	-915-795-3 Sequence	8-915-795-5 Sequence	d 6-96	19-9 Patent No.	-125-642C-15 Sequence 3	-431-888-11 Sequence 1	-431-888-2 Seguence 2	596-17 Patent No.	17 Patent No.	739-18 Patent No.	.3 Patent No.	.5-795-9 Sequence	.5-795-8 Seguence 8.	8-586-039B-33 Sequence 33.	9-699-769-33 Sequence 33,	8-469-427A-15	8-569-063C-20 Sequence 20,	-31 Sequence 31,	-699-769-31 Seguence 31.	8-586-039B-35 Sequence 35	9-699-769-35 Sequence 35.	8-742-243-43 Seguence 43.	8-742-243-44 Sequence 44.	
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	Query Match Length	0	0	9	325	S	120	120	132	132	133	164	164	164	190	321	358	146	4	189	190	σ	σ	214	-	12		
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	Score	55	52	52	52	22	45	45	45	45	45	45	45	45	45	45	45	42	42	42	42	42	42	42	42	41	41	
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RESULT 2

Sequence 3, Appli Sequence 11, Appl	Sequence 11, Appl Sequence 17, Appl	Sequence 10, Appl Sequence 11, Appl Patent No 5194596	22,	sequence 15, Appl Sequence 17, Appl	16,	Sequence 2, Appii Sequence 2, Appli	Sequence 2, Appli	Sequence 4, Appli		4
US-08-691-794-3 US-09-392-932-11	US-09-822-270-17 US-09-342-931-10	US-09-392-931-11 5194596-19	5219739-20	US-09-03/-983C-15 US-09-037-983C-17	US-09-037-983C-16	US-08-784-551C-2	US-09-392-932-2	US-09-574-708A-4 US-09-037-983C-2	US-09-428-909A-2	US-09-392-931-4
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110	110	110	121	137	138	145	145	145 145	145	145
2. 4. 4. 5. 5. 5. 5. 5. 5. 5. 5. 5. 5. 5. 5. 5.	7. 4. 5	74.5	7. T.	.5.	4. 4 r. r.	5.5	٠. دن ر	4. 4. v. r.	4.5	74.5
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288 299	31	. 6. 6. 1. 6. 4.	35	37	38	4	41	4.4. 2.6.	44	45

## ALIGNMENTS

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Gaps
                                                                    GENERAL INFORMATION:
APPLICANT: ACHEN, Marc G.
APPLICANT: STACKER, Steve A.
TITLE CANT: STACKER, Steve A.
TITLE OF INVERTION: ANTHODIES TO TRUNCATED VEGF-D AND USES THEREOF FILE REPERENCE: ACHEN et al-1064-44660
CURRENT APPLICATION NUMBER: US/09/469,186
CURRENT FILING DATE: 1999-12-21
EARLIER FILING DATE: 1998-12-21
EARLIER FILING DATE: 1998-12-21
EARLIER PILING DATE: 1998-05-17
NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 55; DB 4; Length 109; Best Local Similarity 100.0%; Pred. No. 0.15; Matches 9; Conservative 0; Mismatches 0; Indels
                           Sequence 1, Application US/09469186
Patent No. 6383484
                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-09-469-186-1
US-09-469-186-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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53 CCNEESLIC 61 6 1 CCNEESLIC Dp à

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APPLICANT: ACHEN, MAIC G.
APPLICANT: ACHEN, MAIC G.
APPLICANT: STACKER, Steve A.
TITLE OF INVENTION: ANTIBODIES TO TRUNCATED VEGF-D AND USES THEREOF FILE REPERBNCE: ACHEN et al.-1064-44660
CURRENT APPLICATION NUMBER: US/09/469,185
CURRENT FILING DATE: 1999-12-21
EARLIER APPLICATION NUMBER: 60/113,254
EARLIER PILING DATE: 1998-12-21
EARLIER PILING DATE: 1998-05-17
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PATCHIN US: 1 US-09-469-185-1 ; Sequence 1, Application US/09469185 ; Patent No. 6531185 ; GENERAL INFORMATION:

SEQ ID NO 1

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US-08-915-795-5
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APPLICANT: Wise, Lyn M
APPLICANT: Wise, Lyn M
APPLICANT: Savory, Loreen J
APPLICANT: Savory, Loreen J
APPLICANT: Stephen B
APPLICANT: Fleming, Stephen B
APPLICANT: Fleming, Stephen B
TITLE OF INVENTION: VASCULAR ENOTHELIAL GROWTH FACTOR-LIXE PROTEIN FROM ORF
TITLE OF INVENTION: VIRUS NZ2 BINDS AND ACTIVATES MAMMALIAN VEGF
FILE REFERENCE: Sequence Listing for 09/431,833
Patent No. 6541008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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; Sequence 3, Application US/08915795
; Patent No. 6235713
; Patent No. 6235713
; GENERAL INFORMATION:
APPLICANT: Marc G. ACHEN
APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH PACTOR
; MUNGER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
                                                                                  100.0%; Score 55; DB 4; Length 109; nilarity 100.0%; Pred. No. 0.15; Conservative 0; Mismatches n. Trans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 55; DB 4; Length 197; 100.0%; Pred. No. 0.25; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/431,888A CURRENT FILING DATE: 1999-11-02
BARLIER APPLICATION NUMBER: 60/106,689
BARLIER FILING DATE: 1998-11-02
BARLIER APPLICATION NUMBER: 60/106,800
BARLIER FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DC: United States of America
                                                                                                                                                                                                                                                                                                                US-09-431-888-8
; Sequence B, Application US/09431888A
; Patent No. 6541008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 CCNEESLIC 77
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US-09-431-888-8
             TYPE: PRT
CRGANISM: Homo sapiens
US-09-469-185-1
                                                                                                                                                                                                                                53 CCNEESLIC 61
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                                                                                                    Query Match
Best Local Similarity
Matches 9; Conserv
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LENGIH: 109
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Gaps
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APPLICANT: MARCH F. WILKS
APPLICANT: Steven A. STACKER
APPLICANT: Kari ALITALO
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
STREET: 1200 G Street, NW, Suite 700
CITY: Washington
STATE: DC
COUNTRY: United States of America
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 55; DB 3; Length 325; 100.0%; Pred. No. 0.4; tive 0; Mismatches 0; Indels
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,795
FILING DATE:
CLASSITCATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: BYANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/42983
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 107028-88000
TELEFRAX: (202) 628-8800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08915795
Patent No. 6235713
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 536
ATTORNEY AGENT INFORMATION:
NAME: EVANS, JOSeph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064
TELECOMMUNICATION:
TELECHONE: (202) 628-8800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202,
TELEX: N/A
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
. TAMPTH: 354 amino acids
                                                                                                                                                                                                                                                           TELEKIN/
TELLEX: N/A
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
TISSUE TYPE: Human Breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 100.
Lag 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 CCNEESLIC 124
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                                                                                                                                                                                                                                                                                                                                                                                                                linear
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69 CCNDESLEC 77
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ORIGINAL SOURCE:
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                                                  US-09-125-642C-15
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US-09-431-888-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: TISCHER, EDMUND G.;ABRAHAM, JUDITH A.;FIDDES,
JOHN C.;MITCHELL, RICHARD L.
JUDIN C.;MITCHELL, RICHARD L.
JUDIN C.;MITCHELL, RICHARD L.
JUDIN C.;MITCHELL, RICHARD L.
JUDIN C.;MITCHELL, RICHARD L.
JUDIN C.;MITCHELL, RICHARD L.
JUDIN C. FAULTON TON SEQUENCES ENCODING BVEGF120 AND HVEGF121
JUDINGER COF SEQUENCES: 40
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/07/559,041
FILING DATE: 27-JUL-1990
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 450,883
FILING DATE: 14-DEC-1989
APPLICATION NUMBER: 387,545
FILING DATE: 27-JUL-1989
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0
                                                                                                                                                                                                                                                                                                                 RESULT 6
5194596-9
;Patent No. 5194596
; APPLICANT: TISCHER, EDMUND G.;ABRAHAM, JUDITH A.;FIDDES, JOHN
; PICHARD L.
                                                                                                                                                        Query Match 100.0%; Score 55; DB 3; Length 354; Best Local Similarity 100.0%; Pred. No. 0.43; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.8%; Score 45; DB 6; Length 120; 77.8%; Pred. No. 4.9; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                           GROWTH FACTOR

GROWTH FACTOR

MUMBER OF SEQUENCES: 32

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/450,883

FILING DATE: 14-DEC-1989

PRIOR APPLICATION DATE:

APPLICATION NUMBER: 387,545

FILING DATE: 27-JUL-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.8%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Query Match
Best Local Similarity 77.00,
                                                                                    ; ORIGINAL SOURCE:
; TISSUE TYPE: Human Lung
US-08-915-795-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 77.6
Matches 7; Conservative
             STRANDEDNESS: single
TOPOLOGY: linear
                                               MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                              145 CCNEESLIC 153
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amino acid
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;Patent No. 5219739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO:9:
; LENGTH: 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO:9:
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Patent No. 6541008
GENERAL INFORMATION:
APPLICANT: Wise, Lyn M
APPLICANT: Mise, Loren J
APPLICANT: Fleming, Stephen B
APPLICANT: Fleming, Stephen B
APPLICANT: Stacker, Stephen
TITLE OF INVENTION: VASCULAR ENOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF
TITLE OF INVENTION: RECEPTOR-2, AND USES THEREOF
TITLE OF INVENTION: RECEPTOR-2, AND USES THEREOF
FILE REFERENCE: Sequence Listing for 09/431,833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Sequence 15, Application US/09125642C
Patent No. 6365393
GENERAL INFORMATION:
APPLICANT: BAYER AG
TITLE OF INVENTION: Parapoxviruses Which Contain Foreign DNA, a
                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/125,642C
FILING DATE: 20-Aug-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.8%; Score 45; DB 4; Length 132; 77.8%; Pred. No. 5.3; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/EP97/00729, FILING DATE: 17-Feb-97 INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/431,888A CURRENT FILING DATE: 1999-11-02 EARLIER APPLICATION NUMBER: 60/106,689 EARLIER FILING DATE: 1998-11-02 EARLIER APPLICATION NUMBER: 60/106,800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: Parapox ovis
; STRAIN: D1701 VEGF- Protein
US-09-125-642C-15
                                                                                                                                                      NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bayer Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 132 amino acids
                                                                                                                                                                                                                                     STREET: 100 Bayer Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                             CITY: Pittsburgh
STATE: Pennsylvania
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 81.8
Best Local Similarity 77.8
Matches 7; Conservative
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81.8%;
                    Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                        59 CCNDESLEC 67
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                                                                                                   1 CCNEESLIC 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; SEQ ID NO:17:
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; Patent No.
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| Sequence 2, Application US/09431888A
| Sequence 2, Application US/09431888A
| Patent No. 6541008
| GENERAL INFORMATION:
| APPLICANT: Wise, Lyn M
| APPLICANT: Mercer, Andrew A
| APPLICANT: Stacker, Stephen B
| APPLICANT: Stacker, Stephen B
| APPLICANT: Stacker, Stephen B
| APPLICANT: Stacker, Stephen B
| APPLICANT: Stacker, Stephen B
| APPLICANT: Stacker, Stephen B
| APPLICANT: Stacker, Stephen B
| APPLICANT: Stacker, Stephen B
| APPLICANT: Stacker, Stephen B
| APPLICANT: Stacker, Stephen B
| TITLE OF INVENTION: VIRUS NZ2 BINDS AND ACTIVATES MAWMALIAN VEGF
| TITLE OF INVENTION: STECHEN BENEBORE: Sequence Listing for 09/431,833
| Patent No. 6541008
| CURRENT PELING DATE: 1999-11-02
| EARLIER APPLICATION NUMBER: 60/106,689
| EARLIER PILING DATE: 1998-11-03
| NUMBER OF SEQ IN OSS: 11
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APPLICANT: ITSCHER, EDMUND G.; ABRAHAM, JUDITH A.; FIDDES, JOHN
C.; MITCHELL, RICHARD I.
G.; MITCHELL, RICHARD I.
GROWTH FACTOR
NUMBER OF SEQUENCES: 32
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/450,883
FRIOR APPLICATION DATA:
FRIOR APPLICATION DATA:
                                                                                                                                                                        81.8%; Score 45; DB 4; Length 132; 77.8%; Pred. No. 5.3; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.8%; Score 45; DB 4; Length 133; 77.8%; Pred. No. 5.3; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 387,545
FILING DATE: 27-JUL-1989
EARLIER FILING DATE: 1998-11-03
                  NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                          Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                69 CCNDESLEC 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCNDESLEC 78
                                                                                                                                                                                                                                                         1 CCNEESLIC 9
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                                                                           | LENGTH: 132
| TYPE: PRT
| ORGANISM: Orf virus
| US-09-431-888-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
CORGANISM: Orf virus
US-09-431-888-2
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;Patent No. 5194
; APPLICANT:
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                                             Gaps
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5219739-17
FPATENT NO. 5219739
JOHN C. STIPTION T. TISCHER, EDMUND G.;ABRAHAM, JUDITH A.;FIDDES,
JOHN C.;MITCHELL, RICHARD L.
TITLE OF INVERTION: DNA SEQUENCES ENCODING BUEGF120 AND
HUMBER OF SEQUENCES. 40
JUNBER OF SEQUENCES. 40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/559,041
FILING DATE: 27-JUL-1990
PRIOR APPLICATION DATA:
PILING DATE: 14-DEC-1989
JELLING DATE: 14-DEC-1989
JELLING DATE: 27-JUL-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: TISCHER, EDMUND G.;ABRAHAM, JUDITH A.;FIDDES,
JOHN C.;MITCHELL, RICHARD L.
JUDITH A.;FIDDES,
JUDITH A.;FIDDES,
JUDITHE OF INVENTION: DNA SEQUENCES ENCODING BURGF120 AND
HUGGF 121 AND METHODS FOR THE PRODUCTION OF BOVINE AND HUMAN
JVAASCULAR ENDOTHELLAL CELL GROWTH FACTORS, BVEGF120 AND HVEGF121
NUMBER OF SEQUENCES: US/07/559,041
FILING DATE: 27-JUL-1990
PRIOR APPLICATION NUMBER: US/07/559,041
FILING DATE: 14-DEC-1989
HILLOG DATE: 14-DEC-1989
HILLOG DATE: 27-JUL-1989
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Score 45; DB 6; Length 164;
Pred. No. 6.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6; Length 164;
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                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.8%; Score 45; DB 6 77.8%; Pred. No. 6.4;
                                           1; Mismatches
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APPLICANT: FERRARA, NAPOLEONE; LEUNG, DAVID W.H.

TITLE OF INVENTION: PRODUCTION OF VASCULAR ENDOTHELIAL CELL
GROWTH FACTOR AND DNA ENCODING SAME
WUMBER OF SEQUENCES: 15
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/389,722
FILING DATE: 04-MQL-1989
PRIOR APPLICATION NUMBER: 369,424
FILING DATE: 21-UN-1989
FILING DATE: 21-UN-1989
FILING DATE: 12-MAY-1989
                                                                                                                                                                                                                                                                                                                                                                    81.8%; Score 45; DB 6; Length 190; 77.8%; Pred. No. 7.3; ative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
STREET: 1200 G Street, NW, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45; DB 3; Length 321; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United States of America
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/915,795
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US-08-915-795-9
US-08-915-795-9
Sequence 9, Application US/08915795
Fatent No. 6235713
APPLICANT: Marc G. ACHEN
APPLICANT: Andrew F. WILKS
APPLICANT: Steven A. STACKER
APPLICANT: Steven A. STACKER
APPLICANT: Steven A. STACKER
APPLICANT: Steven A. STACKER
APPLICANT: Steven A. STACKER
APPLICANT: Steven A. STACKER
APPLICANT: Steven A. STACKER
APPLICANT: Steven A. STACKER
CORRESPONDENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 536
ATTORNEY/ACENT INFORMATION:
NAME: EVANS, JOSEPH D. C. 269
RECISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064,
TELECHONEI: (202) 628-8800
TELEPHONE: (202) 628-884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (202) 628-8844
TELEX: N/A
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 321 amino acids
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
TISSUE TYPE: Mouse Lung
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 77.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |||:||| |
85 CCNDESLEC 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington STATE: DC
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                  LENGTH: 190
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81.8%; 66.7%;

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Gaps
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  Indels
  ;
 Mismatches
                                                                                Search completed: September 5, 2004, 10:21:58 Job time: 8 secs
 .;
 6; Conservative
                                             145 CCNEEGVMC 153
                       1 CCNEESLIC 9
Matches
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